



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 111055**

**TO: Jeffrey Parkin**  
**Location: cm1/8e15/8e12**  
**Art Unit: 1648**  
**Friday, January 02, 2004**

**Case Serial Number: 08/573569**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**CM1-6A04**  
**Phone: 308-3534**

**toby.port@uspto.gov**

### **Search Notes**

Dear Examiner Parkin,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

STIC-Biotech/ChemLib

CRFE

111055

From: Parkin, Jeffrey  
Sent: Friday, December 26, 2003 8:18 PM  
To: STIC-Biotech/ChemLib  
Subject: U.S. Serial No. 08/573,569

Please search **SEQ ID NO 15** from **08/573,569** (Maassab, H. F., et al.) v. all relevant databases, including interference. Place results on both paper and disk. Thanks!

JSP  
Au 1648  
CM01-8E15  
308-2227

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 15:31:30 ; Search time 8369 Seconds

(without alignments)  
11443.355 Million cell updates/sec

Title: US-08-573-569-15

Perfect score: 2341  
Sequence: 1 AGCGAAGAGCAGGCAUUAU.....AAAAGACCCUUGUUCUACU 2341

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

1 number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_ov:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_scs:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pin:\*  
35: em\_hcg\_rod:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcgo\_hum:\*  
40: em\_hcgo\_mus:\*  
41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2325	99.3	2341	14	FLAPB2A	M23970 Influenza A
2	2313.8	98.8	2341	14	FLAPB2PRO	M81575 Influenza A
3	2312.2	98.8	2341	14	FLAPB2PROA	M81581 Influenza A
4	2309	98.6	2341	6	AX399724	AX399724 Sequence
5	2309	98.6	2341	6	FLAPB2PROB	M81587 Influenza A
6	2305.8	98.5	2341	14	FLAH2NP2A	M73521 Influenza A
7	2332.2	95.4	2341	14	FLAH2NP2B	M73524 Influenza A
8	2217.8	94.7	2341	14	IAPB247	X99053 Influenza A
9	2213	94.5	2341	14	IAPB247MA	X99056 Influenza A
10	2191.4	93.6	2329	14	FLAPB2B	M91713 Influenza A
11	2184.2	93.3	2341	14	FLAP3MOA	J02140 Influenza A
12	2182.6	93.2	2341	14	INA564804	AJ564804 Influenza
13	2173	92.8	2341	6	AX350184	AX350184 Sequence
14	2167.4	92.6	2329	14	FLAP2A	M91712 Influenza A
15	2159.4	92.2	2313	14	AF348170	AF348170 Influenza A
16	2156.2	92.1	2313	14	AF348171	AF348171 Influenza A
17	2129.8	91.0	2341	14	FLAPB2L	M38277 Influenza A
18	2115.4	90.4	2341	14	INFLX1	V00603 Influenza A
19	2113.8	90.3	2341	14	AF389115	AF389115 Influenza A
20	2110.6	90.2	2341	14	AB036782	AB036782 Influenza A
21	2110	90.1	2302	14	AF251394	AF251394 Influenza A
22	2104.2	89.9	2341	14	FLAP2CHILE	M27684 Influenza A
23	2104.2	89.9	2341	14	ORINPB2	X15283 Influenza A
24	2099.4	89.7	2341	14	IAU62543	U62543 Influenza A
25	2096.2	89.5	2341	14	AF258842	AF258842 Influenza A
26	2088.2	89.2	2341	14	FLAP3M	J02179 Influenza A
27	2086.6	89.1	2341	14	FLAH3NP2	M73517 Influenza A
28	2077	88.7	2341	14	INA564805	AJ564805 Influenza A
29	2043.4	87.3	2341	14	AF258524	AF258524 Influenza A
30	2038.6	87.1	2341	14	AF258841	AF258841 Influenza A
31	2033.8	86.9	2341	14	AF258525	AF258525 Influenza A
32	2028.8	86.7	2280	14	AF037412	AF037412 Influenza A
33	2028.8	86.7	2311	14	AF251402	AF251402 Influenza A
34	2025.6	86.5	2280	14	IAU71132	U71132 Influenza A
35	2024	86.5	2280	14	IAU71134	U71134 Influenza A
36	2020.8	86.3	2280	14	IAU71135	U71135 Influenza A
37	2019.2	86.3	2280	14	AF483602	AF483602 Influenza A
38	2014.4	86.0	2280	14	AF037413	AF037413 Influenza A
39	2009.6	85.8	2280	14	AF225514	AF225514 Influenza A
40	2006.6	85.8	2280	14	IAU71133	U71133 Influenza A
41	2006.4	85.7	2280	14	AF037414	AF037414 Influenza A
42	2006.4	85.7	2280	14	AF037415	AF037415 Influenza A
43	2006.4	85.7	2280	14	AF037416	AF037416 Influenza A
44	2006.4	85.7	2280	14	AF225516	AF225516 Influenza A
45	2004.8	85.6	2280	14	AF225515	AF225515 Influenza A

## ALIGNMENTS

RESULT 1

FLAPB2A 2341 bp ss-RNA linear VRL 02-AUG-1993

LOCUS Influenza A/Ann Arbor/6/60(H2N2) polymerase basic 2 protein (PB2), segment 1) RNA, complete cds.

ACCESSION M23970 J04349 M23971

VERSION M23970.1 GI:324981

KEYWORDS polymerase; polymerase basic 2.

SOURCE Influenza A virus

ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.

REFERENCE 1 (bases 1 to 2341)

AUTHORS Cox,N.J., Kilame,F., Kendal,A.P., Maassab,H.F. and Naeye,C.

TITLE Identification of sequence changes in the cold-adapted, live





LOCUS	FLAPB2PRO	2341 bp ss-RNA	linear	VRL_12-FEB-2001
DEFINITION	Influenza A virus (A/Leningrad/134/57 (H2N2)) PB2 protein (PB2)			
QY	1381	GAACAUUACGACAUUGUGUGGAAUUGAUUUGGGGUAUUAACGAGACUAUACUCCAAAGCA	1440	
Db	1381	GAACATATGCAATGTGAATGGAAATGATTTGGGGATTTTACAGACATGAATCTCCAAAGCA	1440	
QY	1441	GAGUUGUCAUUAGAGAGGGGUAAAGAGUCACGACAAAUUGGGCGUAGUAAUUAUCUACGCGG	1500	
Db	1441	GAGATGTCAAATGAGAGGGGTAAAGAGTCAAGCAAAATGGCGGTATGAAATTAATCTCCAGCGCG	1500	
QY	1501	GAGAGAGUAGUGUGUGAGCAUUGACCGGUGUUUUGAGUUCGAGACCAACGAGAAUUGUA	1560	
Db	1501	GAGAGAGTGTGTGTGTGAGCATTCACCGGTTTGTGAAGTTCCGAGACCAACGAGGAAATGTA	1560	
QY	1561	CUAACUATCCUCCGAGAGAGGUGUGUAACACAGGGGACAGGAAATCUACAUUAUUAUAC	1620	
Db	1561	CTACTATCTCCCTGAGAGAGGTCAGTGAACACAGGGAACAGGAAATGACAAATTAATCTTAC	1620	
QY	1621	UCAUUGUCUAUAGUUGGGGAGUUAUUGGCCUGAGUGUCAGUUGUGUCAAUAUACUACUAG	1680	
Db	1621	TGATGTGTCAATGAATGTGGAGATTAATGGCCCTGAGTCAAGTGTGTGTCAATACCTATACG	1680	
QY	1681	UGGACAUCAUAGAAACUGGGGAAACUGUUAUAAAUUCCAGUGUGUCUAGAUUCUACAUUCUA	1740	
Db	1681	TGGATCATCAGAAACTGGGAAACTGTAAAAATTCAGTGTGTCAAGAAATCTACATATGCTA	1740	
QY	1741	UACAAUAAAUAUGGAUUAUUGAGCCAUUUCAGUCUUUUAUGUUCUUAAGCCAUUAGAGGCCAA	1800	
Db	1741	TACAAATTAATATGGAAATTTGAGGCCATTTTCAGTCTTTAATGTTCCCTAAGGCCCATTAAGAGGCCAA	1800	
QY	1801	UACAGUGGUGUUGUAGGACUUCUAUUCUCAAACAAUAGAGGAGUAGUUAUUGUGGACAUUUGAU	1860	
Db	1801	TACAGTGGGTTTGTTAAGACTTATATTCCAAACAAATGAGGAGATGATCTTGGGACATTTGAT	1860	
QY	1861	ACCACCCAGAUUAUAAAACUUCUUCUCCUUGUGAGCGGCCCAACCAACAAAGUAGUAUG	1920	
Db	1861	ACCACCCAGATTAATTAACCTTCTTCCTTGGAGCGGCCCAACCAAGAAATGAATG	1920	
QY	1921	CAGUUCUUCUACUCUACUUGUAGUAGGAGAUACAGAAUAGAGAUUAUUCUUGUAAAGGGGC	1980	
Db	1921	CAATTCCTTTCAATTAAGTCAATGTGAATGTGAGGGGATCAGGAATGAGAAATTAATCTGTAAAGGGGC	1980	
QY	1981	AAUUCUCCUUAUUAUUGAACUACCAACGAAGCACUAUAGAGACUUAACAUUUCUGGAAAGGAAU	2040	
Db	1981	AATTTCTCTATATTTAACTAACACAGACCACTAAGAGACTTAACAAATTTCTCGAAAGGAT	2040	
QY	2041	GCUGGACAUUUAACUAGAGACCAGAGUAGAGGCAUUCUGAGUGGAGUCCGUGUUCUG	2100	
Db	2041	GCTGGCACTTTAACTGAAGAGCCCAAGATGAAGGACATCTGGAGTGAAGTCCGCTGTTCTG	2100	
QY	2101	AGAGGAUUCUUCUACUGGGCCAAAGAGAUUAGAGAUUUGACCAAGCAUUAUAGCAUACAU	2160	
Db	2101	AGAGGATTCCTCATTTCTGGGCAAAAGAAATAGAGATATGAGCAGCATTAATTAAGCATCAAT	2160	
QY	2161	GAAUCUAGUAUACCUUGGAGAGAGGAAAGGCUAUAUUGUAGUUGGGCAGAGAGACUG	2220	
Db	2161	GAACTGATTAACCTTTCGAAAGGAGAAAAAGCTTAATGTAAATTTGGCAAGGAGACGTG	2220	
QY	2221	GUGUUGUAUAGAAACGAAAAACGAAACUUCAGUACUUAUCUGACAGCAGACAGCAAC	2280	
Db	2221	GTTGTTGTTAAATGAACGAAAAACGAAACCTCTAGCATTAATCTGACAGCAGACAGCAAC	2280	
QY	2281	AAAAAGAUUCGGAUGGCCAUCACAUUAUUGUAGAUUUAUAAAAACGACCUUGUUCUAC	2340	
Db	2281	AAAAGGATTCGGATGCGCATCAATTAATGTTGAATAGTTAAAAACGACCTTGTTCATC	2340	
QY	2341	U 2341		
Db	2341	T 2341		

	gene, complete cds.
ACCESSION	M81575
VERSION	M81575.2
KEYWORDS	GI:8281016
SOURCE	Influenza A virus (A/Leningrad/134/57 (H2N2))
ORGANISM	Influenza A virus (A/Leningrad/134/57 (H2N2))
REFERENCE	Virus(es); ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus(es); Influenzavirus A; Influenza A virus; H2N2 subtype.
AUTHORS	1 (bases 1 to 2341) Klimov,A.I., Cox,N.J., Yotov,W.V., Rocha,E., Alexandrova,G.I. and Kendal,A.P.
TITLE	Sequence changes in the live attenuated, cold-adapted variants of influenza A/Leningrad/134/57 (H2N2) virus
JOURNAL	Virology 186 (2), 795-797 (1992)
MEDLINE	92124758
PUBMED	1733114
REFERENCE	2. (bases 1 to 2341)
AUTHORS	Klimov,A.I.
TITLE	Direct Submission
JOURNAL	Submitted (20-JAN-1992) Research Institute for Viral Preparations, Academy of Medical Sciences of the USSR, Moscow, USSR
REFERENCE	3 (bases 1 to 2341)
AUTHORS	Klimov,A.I.
TITLE	Direct Submission
JOURNAL	Submitted (06-JUN-2000) Influenza Branch, G-16, Centers for Disease Control and Prevention, 1600 Clifton Rd., Atlanta, GA 30333, USA
REMARK	Sequence updated by submitter
COMMENT	On Jun 6, 2000 this sequence version replaced gi:324995.
FEATURES	location/Qualifiers
source	1..2341
organism	"Influenza A virus (A/Leningrad/134/57 (H2N2))"
molecule	/mol_type="genomic RNA"
strain	/strain="A/Leningrad/134/57 (H2N2)"
db_xref	/db_xref="taxon:128148"
db_xref	28..2307
gene	/gene="PB2"
cds	28..2307
gene	/gene="PB2"
cds	/codon_start=1
product	/product="PB2 protein"
protein_id	/protein_id="AAA19213.2"
db_xref	/db_xref="GI:8281017"
translation	"/translati...MERIKELRLMMSQSRRELILTTTVDHMAIIKKYTSGRGKPKS LRNMAMAKRPIITADKRITEMIPERNBOQTLMSSKSDGSORWVSPPLAVTWNNRN GPMTSTVHPKIYKTFFEKVEERLKHGFVFHFNRDVKIRRDVIDNGHADLSAKEKO DVIMEVVFPEBVGARILITSQSOLRTIFKEKEFLDDCKISPLAVAYMLERILVETREFI PVAGSGSVSYIVLHLTGTCMEOWYTPGCEVANNDVDSLLIAARNIVRAVASAP LASILERCHSTOIGTRMDILFONLPTEBEADVNICCAAMLRISSSESRCGFIFPKRS GSSVKBEEVLGNLOTLAKIRHGEYEFEPVSKRATPAIRKARTLIQLIVSGDRDO SIEBAIVANVFQSOEDCMIKAVAGDLNFVRANQRNPIMQLRHFDKDKAKVLFOMWG IHIDHWGMGIVLPMTPESTEMSMRGVRYSKGVDSESAEERVVSIIDFLRVLDOR GNVLISEPESYSTREKLTIITYSSMGMINDEPSLVNTYOMIIRNMFETVWKIOWMO NPPTMLYNKMFEFPOTGLVPKALINGOYSGFRFTILOMRDVLGTFTPTQILKLPRFAAA PPPOKSROSSLTVNVKSGMRILVRGNSVFENVNKTITKLTILLGDAGLTLEDPDGEG TSGVESVLAENGLFIIGKEDRRXGYPALINELNLAKERGEKANVLIQGGDVLTVMKRRKD SSILTDSQTLTKRIRMAIN"

Db 121 AAGAACTACATCAGGAGACAGAAAAAGAACCCGCTCACTTAGATGAAATGATGATG 180  
 Qy 181 GCAUAGAAUUAUCCGUAUUAACAGCCGACAAAGAGAUUAAGAAUUAUUCUGAGAAU 240  
 Db 181 GCAATGAATATATCCGATTAACGCTGACAAAGAGATTAACGAAATGATTCCTGAGAGAAAT 240  
 Qy 241 GAGCAAGGGCAAACTUCUUAUGAGUAAAAGAGUAGUCCGAGUCCGAGUCCGAGUAGU 300  
 Db 241 GAGCAAGGGCAAACTTATGAGTAAAGATGATGCGGATTCGAGATCGAGATGAGTAA 300  
 Qy 301 UCAUCCUGUGUGUAGUAGUAGUAGAAUAGAACCAUAGCAAGUAGAGGUGUUAU 360  
 Db 301 TCACTCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 Qy 361 CCAAAAATCTACAAAATCTTATTTGAGAAAGTGCAGAAAGTTTAAATCATGAACTTTGGC 420  
 Db 361 CCAAAAATCTACAAAATCTTATTTGAGAAAGTGCAGAAAGTTTAAATCATGAACTTTGGC 420  
 Qy 421 CCUGUCCAUUUUUAAGAACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480  
 Db 421 CCGTCCATTTTAAAGAACCAAGTCAAAATACGCGAAGATTAATCAATTAATCAATTAAT 480  
 Qy 481 GCAAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 540  
 Db 481 GCAAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 540  
 Qy 541 GUGGGGGCCAGAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600  
 Db 541 GUGGGGGCCAGAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600  
 Qy 601 GAACTCCAGAGATGGAATAATTTCTCTTGTGATGTTGGTACATTTTGAAGAGAACTT 660  
 Db 601 GAACTCCAGAGATGGAATAATTTCTCTTGTGATGTTGGTACATTTTGAAGAGAACTT 660  
 Qy 661 GUGCGAAAAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 720  
 Db 661 GUGCGAAAAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 720  
 Qy 721 UUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 780  
 Db 721 UUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 780  
 Qy 781 AAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 Db 781 AAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 Qy 841 GUUAUAGAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900  
 Db 841 GUUAUAGAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900  
 Qy 901 ACAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 Db 901 ACAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 Qy 961 AAGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020  
 Db 961 AAGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020  
 Qy 1021 AGAAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080  
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 Qy 1081 TTGAATAATTAAGGCTCATGAGGATTAACAGAGATTACAAATGTTGGAAAAAGGCAACA 1140  
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 Qy 1201 CAGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1260  
 Db 1201 CAGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1260

Qy 1261 AAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1320  
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 Db 1441 GAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1500  
 Qy 1501 GAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1560  
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 Qy 1561 CUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1620  
 Db 1561 CUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1620  
 Qy 1621 UCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1680  
 Db 1621 UCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1680  
 Qy 1681 UGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1740  
 Db 1681 UGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1740  
 Qy 1741 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1800  
 Db 1741 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1800  
 Qy 1801 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1860  
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 Qy 1861 ACCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1920  
 Db 1861 ACCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1920  
 Qy 1921 CAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1980  
 Db 1921 CAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1980  
 Qy 1981 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2040  
 Db 1981 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2040  
 Qy 2041 GUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2100  
 Db 2041 GUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2100  
 Qy 2101 AGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2160  
 Db 2101 AGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2160  
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QY 2341 U 2341  
Db 2341 T 2341

RESULT 3  
FLAPB2PROA  
LOCUS  
DEFINITION  
Accession  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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Influenza virus type A/Leningrad/134/17/57 (H2N2) PB2 gene,  
complete cds.  
M81581  
GI:8281025

Influenza A virus (A/Leningrad/134/17/57 (H2N2))  
Influenza A virus (A/Leningrad/134/17/57 (H2N2))  
viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza  
A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype.  
1 (bases 1 to 2341)  
Klimov,A.I., Cox,N.J., Yotov,W.V., Rocha,E., Alexandrova,G.I. and  
Kendal,A.P.  
Sequence changes in the live attenuated, cold-adapted variants of  
Influenza A/Leningrad/134/17/57 (H2N2) virus  
Virology 186 (2), 795-797 (1992)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
1733114  
2 (bases 1 to 2341)  
Klimov,A.I.  
Direct Submision  
Submitted (20-JAN-1992) Research Institute for Viral Preparations,  
Academy of Medical Sciences of the USSR, Moscow, USSR  
3 (bases 1 to 2341)  
Klimov,A.I.  
Direct Submision  
Submitted (06-JUN-2000) Influenza Branch, G-16, Centers for Disease  
Control and Prevention, 1600 Clifton Rd., Atlanta, GA 30333, USA  
Sequence updated by submitter  
On Jun 6, 2000 this sequence version replaced gi:324997.  
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BASE COUNT 797 a 415 c 586 g 543 t  
ORIGIN

Query Match 98.8%; Score 2312.2; DB 14; Length 2341;  
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Matches 1786; Conservative 517; Mismatches 18; Indels 0; Gaps 0;

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Db 361 CCAAAAATCTACAAACATTTATTTGAGAAAGTCGAAAGGTTAAACATGAAACCTTTGGC 420  
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QY 481 GCAGACUCUAGUGCCAAAGAGAGCAGAGAUUAUACUAGAAUGUUGUUCUUAACGA 540  
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Qy      1201  CAGUGCAUUGCGUAGCAUAUAUUGUGCGCAUGGUUAUUUUCACAAAGAAUUGUUAUA 1260
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Db      1261  AAGAGAGTTAGAGGTGATCTGAATTTCTTAATAGGCGAAATCAAGCATGAAATCCCATG 1320
Qy      1321  CAUCAAUUUUUAAGCAUUUUUCAGAAAGUAGGAAAGUUGUUUUUUAUUUGGAGAAU 1380
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Qy      1381  GAACAUUUCGACAUUGUAGUUGGAAUUGAUUGGAGUUAUCCAGACAUUGAUUCCAGACA 1440
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Qy      1501  GAGAGAGUAGUGUGAGCAUUGACCGUUUUUUGAGUUGUAGUAGCAACAGAGAAUUGUA 1560
Db      1501  GAGAGAGATAGTGGTGGATGATGACCGGTTTTTGAAGATTCGAGACCAAGAGAAATGTA 1560
Qy      1561  CUACUAUUCUUGAGAGAGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1620
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Qy      1681  UGGAUUCUAGCAAAACUGGAGAAACUGUUAUUUAUUUAGUGUUCUAGAUUCUUAUUGUA 1740
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Influenza A virus (STRAIN A/SINGAPORE/1/57)
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; unidentified
subtype.

REFERENCE
1
Perko,B., Egorov,A., Romanova,V., Katlinger,D. and Katlinger,H.
Live vaccine and method of manufacture
Patent: WO 0224876-A 1 28-MAR-2002;
POLYMON SCIENT IMMUNO BIO FORSCH (AT)
FEATURES
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Qy      121  AAGAAUAGCAUUCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
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Qy      241  GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 300
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Db	1441	GAGATGTCAATGAGAGGGTAAAGATTCAGCAAAATGGCGGTATGAATACTCCAGCGC	1500
QY	1501	GAGAGAUUGUGUGAGCAUUGACCGGUGUUUUGAGAUUCCAGACCAACGAGAAUUGA	1560
Db	1501	GAGAGAUUGUGUGAGCAUUGACCGGUGUUUUGAGAUUCCAGACCAACGAGAAUUGA	1560

Db		1501	GAGAGAGTAGTGTGAGCAATTTACCGGGTTTTTGTAGAATTGCAGACAACAGAGAAATGTA	1560
Oy		1561	CUACUAUUCUCCUGAGAGAGUGUCAUGUAAAACAAGAGAAAACAAGAAACUGAACUAUACUAC	1620
Db		1561	CTACTCATTCCTTGAGAGAGGTGAAGTGAACACAGAGGAAACAAGAAACTTGACATACTTAC	1620
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Db		1621	TGATGTCAATAGATGTGGAGATTAATATGGCCCTGATGTCAGTGTGTCAATATCCTATCAG	1680
Oy		1661	UGGUANCANACAAACUGGGAAAACUGUAAAAAUACAGUGUUCUGAAUUCUCAAUUCUA	1740
Db		1661	TGGATCAACACAAACCTGGGAAAACGTTTAAATTCAGTGTCTCGAAATTCCTACAAATCTA	1740
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Db		1741	TACATATAAAATGGAATTTGAGCCATTTCCAGTCTTAAATTCTTAAGGCCATTAGAGGCCAA	1800
Oy		1801	UAACUGUGGUGUUNUAGACUCUUAUUCCAACAAUAGAGGAUGUAUUUGGACACUUNUGAU	1860
Db		1801	TACAGTGGGTTGTGTAAGGACTCTATTCCAAACAAATGAGGAGATGTAATCTTGAGCAATTGAT	1860
Oy		1861	AACACCACGANAAUAAAACUUCUUCUCCUUGUCAGACCGCCCCCAACAAAGCAAAGUAGAU	1920
Db		1861	ACCAACCCAGATAATPAAAACCTTCTTCCCTTGACACCGCCCCCAACAAAGCAAAGTAGAYG	1920
Oy		1921	CAGUUCUCUCACUGACUCUGAUGAUGUGAGGGGAAUCAGAAUUGAUAUACUUGUUAAGAGGC	1980
Db		1921	CAGTTCTCTTATTTGACTGTGATGTGAGGGGATCAGGAATGAGATATCTTTGTAAGGGCC	1980
Oy		1961	AAUUCUCCUAAUUNUCAAACUACAAACAGACCACUAAAGAGACUAAUUCUCUGAAAGAU	2040
Db		1961	AATTCTCCTGTAATTCACACTAACACAAAGCACCTAAAGAGACTTAACAAATTTCTCGAAAAGAT	2040
Oy		2041	GCUGGCACUUAUACUAGAAAGCCAGANAGAAAGGACCAUUCUGAUGUGAGUCCGUCUUCUG	2100
Db		2041	GCTGGCACTTTTAACTGAAAGCCAGATGAAAGGACATCTGGATGTGAGTCCGCTGTTCTG	2100
Oy		2101	AGAGGAAUUCUUCUAUUCUGGCGAAAGAAAGAAUAGAGAUUGGACACGACUUAUAGCAUCAU	2160
Db		2101	AGAGGATTCCTCATTTCTGGCGAAAGAAAGATATGAGGATATATGACACGACTTAAGCATCAAT	2160
Oy		2161	GAACUGAGUAAACCUUGCGAAAAGAGAAAAGGCUAAUGUAUCUAUUGGGCAAGAGACGUG	2220
Db		2161	GAACTGAGTAACTTTGCGAAAGAGAAAAGGCTAATGATTAATTTGGGCAAGAGAGACGTG	2220
Oy		2221	GUGUGUGUAUAGAAACGAAAACGGAACUCUAGCAUACUACUGACACGACGACGCGACC	2280
Db		2221	GTTGTTGGTAATGAAAACGAAAACGGGACCTTAAGCACTTACTGTGACACGACGACGACCC	2280
Oy		2281	AAAAGGAUUGGAGUAGGCCCAUCAUUAUUVUUGAUAUAGUUAUAAAACGACCUUGUUCUAC	2340
Db		2281	AAAAGGAATTCGGATGGCCATCATTAATTATGTTGAATAGTTTAAAAAACGACCTTGTTCAC	2340
Oy		2341 U 2341		
Db		2341 T 2341		
RESULT 5				
FLAPB2PROB				
LOCUS	FLAPB2PROB	2349 bp ss-RNA	linear	VRL_12-FEB-2001
DEFINITION	Influenza A virus (A/Leningrad/134/47/57 (H2N2))	PB2 protein (PB2)		
KEYWORDS	gene, complete cds.			
ACCESSION	M81587			
VERSION	M81587.2 GI:8281033			
SOURCE	Influenza A virus (A/Leningrad/134/47/57 (H2N2))			
ORGANISM	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype.			
REFERENCE	(bases 1 to 2349)			
AUTHORS	Klimov,A.I., Cox,N.J., Yocovov,M.V., Rocha,E., Alexandrova,G.I. and			





OY		1381	GAAAGCAUUGGACAUUCUGAUAUGGGGAUAUAUTUGGGGUUUUACAAGACUAUCAUCUCCAGCACCA	1440
Db		1381	GAACTATCATGACATATGTGATGGGAAAGAATTGGGGATTTTACAGAGACATGACTCCMAAGCACA	1440
OY		1441	GAGAUUCUAUGAGAGAGGGGUAGAAGUCACAAAUAUUGGGGUGUGAUGAUAUUCUCCAGCGCG	1500
Db		1441	GAGATTCCTCAATGAGAGGGTTTAAGAGTGACAGAAAATGGGGTGTGATGATACTCTCCAGAGCG	1500
OY		1501	GAGAGAUUGUGUGUGAGCAUUGACCCGGUUUUUGAGUUCGAGACCAAAGAGAAUAUUA	1560
Db		1501	GAGAGAGTAGTGGTGAGCAATTGACCGGTTTTTTGAGAGTTTCAGAGCCAACGAGGAAATGTGA	1560
OY		1561	CUAUCUUAUCUCUGAGAGAGUCAGUGAAACAACAGGGACAAGAGAACTUGACAUAACTUAC	1620
Db		1561	CTATTATCTCTTGAGAGAGGTCAAGTAAACAAGGAAACAGAGAACTGACAAATTAATCTTAC	1620
OY		1621	UCAUCGUCUAUUGAUGUGGAGAUUAUUGGCCUGUGUCAGUGUUGUGUCUAUUCUAUUCAG	1680
Db		1621	TCAATCCTCAATGATGTGGAGATTAATGACCCTGAGTCAAGTGTGTGCATAATCCATATCAG	1680
OY		1681	UGGCAUUCACAGAAACUGGGGAAACUGUUAAAAUUCAGUGUGUCUACAAUUCUACAUUGCUA	1740
Db		1681	TGGATCATCAGAAACTGGGAAACTGTGTAATAATTCAGTGGTCTCAGAAATCTTACATGCTA	1740
OY		1741	UAACAUAUAAUUGGAUUAUGGCCAUUUCAGUCUUUUAUGUUCUUAAGCCAUUUAAGGCCAA	1800
Db		1741	TACAAATTAATAATGGAAATTGAGCCATTTTCAGTCTTTAGTTCCTAAGGCCATTTAGAGGCCAA	1800
OY		1801	UACAGUGGGUUGUUGAGACUCUAUUCCAAAGAAUAGAGGAAUUAUUCUUGGACAUUUGCAU	1860
Db		1801	TACAGTGGGTTTGTTTGAAGACTCTATTCCAAACAAATGAGAGGATGTACTTGGGACATTTGAT	1860
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Db		1861	ACCAACCCAGATATATATAAACTTCTCCCTTGTGAGCGCGCCCCAACAAAGTAATGAAATG	1920
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Db		1921	CAGTTCCTCTTCAATTGACTGTGAATGTGAGGGGATTCAGGAAATGAGAAATCTTGTAAAGGGC	1980
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Db		2041	GCTGSCACTTTAATCGAAGAACCCAGCATGAAAGGCACTCTGGAATGTGACTCCGCTGTTCTG	2100
OY		2101	AGAGGAUUCUCUACUUCUGGGCAAAGAGAGUAUGAGAUUUGSACCAAGCAUUAUAGCAUCAU	2160
Db		2101	AGAGGATTCCTCATATTCTGGGCAAAGAMAGATGAGAGATGTGAGACCAAGCATTAAGCATCAAT	2160
OY		2161	GAAUCGAAUAAACCUUGCGAAAGAGAAAGCCUAUUGUAUAUUGGGCCAAAGAGAGUG	2220
Db		2161	GAACTGAAATACCTTGGCCAAAGAGAAAGAAAGGCTAAATGTACTAATTTGGCCAAAGAGAGCTG	2220
OY		2221	GUGUUGUGAUAUGAAACGAAAAACGAAACUCUAGCAUUAUCUGACAGGACGAGCGACC	2280
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OY		2341	U	2340
Db		2341	T	2341

RESULT 6  
FLAH2N2P2A                      2341 bp ss-RNA                      linear                      VRL 02-AUG-1993

LOCUS                                  FLAH2N2P2A

DEFINITION                      Influenza A/Singapore/1/57 (H2N2), PB2 polymerase, complete cds.

[illegible]

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Db	421	CTGTGCCATTTTAGAAGCAACAGTCAAATATACCGCGAAGAGTTGACATTAATCCCTGGCAT	480
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Db	541	GUGGGGGCCAGGATCTACTACGTCCGAAATCCGCAATTAACATTAACCAAGAAAGAAAAGAA	600
QY	601	GAACTCCAGAGATTCGAAAAATTTCTCTTGGATGGTTGGGTACAGTTTAAAGAGAACTT	660
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QY	661	GUCCGAAACAGAGATUUUCUCCCAUUCUGUGUGAACAACAGUUGUAUAUUGAAAGUG	720
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QY	841	GUUAUACAGACAGUCCACUAGCAUCUUUAUUGAGAGUGGCGCACAGACACAGAUUGGCGGG	900
Db	841	GTAATACAGAGATCCACTACGACTCTTTATTGGAGATGTGCCACAGACACAAATTTGGGGG	900
QY	901	ACAAGAGUUGUGGAGCAUUCUUAGGCAAAACCCACAGAAAGACAAACGUCUGGAAUAUUGC	960
Db	901	ACAAAGATGCTGGAATCTTATGGCGAAGAACCCAAACGAAAGACAAAGCTGTGCAATATATGC	960
QY	961	AAGGUGCAUUGGGACUCAGAGUCCAGUCCUACUUGUGGCGGGUUCACAUUUUAG	1020
Db	961	AAGGCTGCATATGAGACTGAAAAATCAGCTCATCTTCAAGTTTGGCGGGTTCACTTTAAG	1020
QY	1021	AGAAACAGCGGACUACUACAGUCCAAAGAGAGAGAAAGAGUGUCUACCGGCAUUCUCAAACA	1080
Db	1021	AGAAACAGCGGATCATACGTCAAGAGAGAGAAAGAAATGCTTACCGGCAATCTTCAAACA	1080
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Db	1081	TTGAAAAATTAAGGCTGATGAGGAAATACGAGAGTTCAACAATGGTGTGGAAAAAGGCAACA	1140
QY	1141	GCUAUAUCUAGAAAAAGCAACGAGAGAUUGAUUACUGAUUGUGUGAGGCAAGACGAA	1200
Db	1141	GCTATATCTAGAAAAGCAACGAGAAATGTAATTCAGCTGATATGTAAGTGGAAAGACGAA	1200
QY	1201	CAGUCGUAUAGCUGAAGCAUAUAUUGUGGCCCAUGUGUAUUUUCACAGAAAGUUGUAUUA	1260
Db	1201	CAGTCGATAGCCGAAGCAATTAATTTGGCGCAATGTAATTTTTCACAAAGAAATTTGATGATA	1260
QY	1261	AAGCAGUUAAGAGUUCUACUAUUUUGUAUUAUUGGCGAAUACAGAGAUUGAAUUCGAG	1320
Db	1261	AAGGCGATTAGAGGTGATCTGAATTTTCGTTAATAGGACAAATCAGGATTTGAATCCCATG	1320
QY	1321	CAUCAAACUUUUUAGACAUUUUCAGAAAGUCCGAAAGUGCCUUUUUCAAUAUUUGGGGAUU	1380
Db	1321	CATCAACCTTTTAAGACATTTTTCAGAAAGATGCGAAAGTCTTTTCAAAAATTTGGGGAATT	1380
QY	1381	GAAACAUUAGACAUUGUGAUAUUAUUGGAAUAUUGUGGUUAUUCAGACACUACUCCAGACCA	1440
Db	1381	GAAACATATGACAAATGTGAGATGATTTGGGATTTTACAGACATGACTCCAAAGACCA	1440

[illegible]



ORGANISM	Influenza A virus
REFERENCE	Viruses; sRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
AUTHORS	1 (bases 1 to 2341)
TITLE	Gorman, O.T., Donis, R.O., Kawachi, Y., and Webster, R.G.
JOURNAL	Evolution of influenza A virus PB2 gene: implications for evolution of the ribonucleoprotein complex and origin of human influenza A virus
MEDLINE	J. Virol. 64 (10), 4893-4902 (1990)
PUBMED	90376444
COMMENT	2398532
FEATURES	Original
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BASE COUNT	811 a 422 c 574 g 534 t
ORIGIN	
Query Match	95.4%; Score 2232.2; DB 14; Length 2341;
Best Local Similarity	74.6%; Pred. No. 0;
Matches 1746; Conservative 527; Mismatches 68; Indels 0; Gaps 0;	
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	1 AGCAAAAGCAGGTCACATTATTTTCACATATYGAAAGAAATTAAGAAACATACGGAATCTGATG 60
Y	61 UCGCAGUCUGCCACUCGCGAGAUUUAUCAAACAAACACAGUGAGCAUUGGCCAUUAU 120
Db	61 TCGCAGTTCGCCACTCGCGAATATCTACAAACAAACCAAGTGGACCATATGATTT 120
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Y	361 CCAAAAATCTCAAGAGCTTATTTGAGAAAGTCAAAAGGTTAAAACTGGAAACCTTTGGC 420
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Db	421	CTGTGTCATTTTAAAGAACCAAGTCAAAATACGCCCAAGAGTTGACATTAACCTCTGTCAT	480
QY	481	CGAGACCTUCAGUGCCCAAGAGGACACAGAGUUAUAUCAUGGAAGUGUUGUUCUCCUAAACGA	540
Db	481	GGAGACCTCAGTGGCCAGAGGCGACAAACGTAAATCATGGAAAGTTGTTTCCCAATGAA	540
QY	541	GUGGGGGCCAGGUAUCUAAACGUCGGAUUCGCAUUTUACAUAUACCAAGAGAAAAAGAA	600
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QY	601	GAACTUCACGAGUUGUGAAAUAUUUCCCUUGUAGUGUGUGUUGUUAUUGAGAGAAACUU	660
Db	601	GAACTCCCAAGANTGCAAAAATTTCTCTTGGATGGTTGGATACATGTTAGAGAGAAACTT	660
QY	661	GUCCGCAAAAAACGAGAUUUCUCCCGAGUUCUGUGGGAACAACAGUGUGUACAUUGAGUG	720
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QY	721	UUGCACUUGACUCACAGAAACUUGCGGGAAACAUGUACACUCCAGUGUGAGAAUGAGG	780
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QY 1861 ACCACCCAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1920
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QY 1921 CAGUUCUUCUACUGAGUGUGAGUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
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QY 2341 U 2341
Db 2341 T 2341

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RESULT 8
IAPB247
LOCUS IAPB247 2341 bp RNA linear VRL 07-MAY-2003
DEFINITION Influenza A virus (STRAIN A/FORT MONMOUTH/1/47) PB2 gene for
POLYMERASE basic protein 2, genomic RNA.
ACCESSION X99035.1 GI:1430834
VERSION PB2 gene; polymerase basic protein 2.
KEYWORDS Influenza A virus (STRAIN A/FORT MONMOUTH/1/47)
SOURCE Influenza A virus (STRAIN A/FORT MONMOUTH/1/47)
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; unidentified

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REFERENCE
AUTHORS Smeenk, C.A., Wright, K.E., Burns, B.F., Thaker, A.J., and Brown, E.G.
TITLE Mutations in the hemagglutinin and matrix genes of a virulent
Influenza virus variant, A/FM/1/47-Ma, control different stages in
pathogenesis
JOURNAL JOURNAL
MEDLINE 9703391
PUBMED 8879138
REFERENCE 2 (bases 1 to 2341)
AUTHORS Brown, E.G.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) E.G. Brown, University of Ottawa, Dept of
Microbiology & Immunology-Faculty of Medicine, 451 Smyth Rd,
Ottawa Ontario K1H 8M5, CANADA
Location/Qualifiers
FEATURES
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QY 61 UCCGAGUCUGGAGCUGGCGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 120
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REFERENCE 1  
 Smeenk, C.A., Wright, K.E., Burns, B.F., Thaker, A.J. and Brown, E.G.  
 Mutations in the haemagglutinin and matrix genes of a virulent  
 Influenza virus variant, A/FM/1/47-MA, control different stages in  
 pathogenesis  
 JOURNAL Virology 44 (2), 79-95 (1996)  
 MEDLINE 97033391  
 PUBMED 8879138  
 REFERENCE 2 (bases 1 to 2341)  
 Brown, E.G.  
 Direct Submision  
 Submitted (03-JUL-1996) E.G. Brown, University of Ottawa, Dept of  
 Microbiology & Immunology, Faculty of Medicine, 451 Smyth Rd,  
 Ottawa Ontario K1H 8M5, CANADA  
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FEATURES  
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CDS

1 (bases 1 to 2329)  
 Lawson, C.M., Subbarao, E.K. and Murphy, B.R.  
 Nucleotide sequence changes in the polymerase basic protein 2 gene  
 of temperature-sensitive mutants of influenza A virus  
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QY 1627 UCAUAGAGUGGAGAUUAUUGCCCUAGUACUGUUGUGUCAAUAACUUAAGUGAUC 1686  
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RESULT 11  
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LOCUS





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RESULT 12
LOCUS   INAS64804
DEFINITION   Influenza A virus (A/PR/8/34 (H1N1) x A/England/93/69 (H3N2)) mRNA
ACCESSION   AJ564804

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VERSION AJ564804.1 GI:314442132
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REFERENCE  1 Pappworth, I. Y.
            Studies in Influenza A virus induced apoptosis
            Unpublished
            2 (bases 1 to 2341)
AUTHORS    Pappworth, I. Y.
TITLE      Direct Submission
JOURNAL    Submitted (29-MAY-2003) Pappworth I. Y., Bioscience, The university
            of Birmingham, Edgbaston, Birmingham, B15 2TT, UNITED KINGDOM
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[illegible]

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D	b	901	ACAAAGATGCTGGACATTCTTAGGCAAAACCCGACGAAAGAACAGCTGTGGATATATGTC	960
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D	b	1021	AGAAACAACGGGATCATCATCTCAAAAGAGAGAGAAAGTCTTACGGGCAATCTTCAACA	1080
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D	b	1201	CAGTCAATATGCGAAGCGATTAATTGTAGTCATGCTGTTTTCACAAAGAGATTCAGATGTA	1266
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[illegible]

JOURNAL MEDLINE	PubMed	COMMENT	FEATURES	source
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[illegible]







GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: December 31, 2003, 15:29:54 ; Search time 605 Seconds

(without alignment)  
10445.264 Million cell updates/sec

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15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*

16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*

17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*

18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*

19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*

20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*

21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*

22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*

23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2309	98.6	2341	24	AAD37054
2	2173	92.8	2341	24	ABR3934
3	2110.6	90.2	2341	20	AAK82192
4	2094.6	89.5	2341	18	AAT75688
5	2093	89.4	2341	18	AAT75690
6	2091.4	89.3	2341	18	AAT75686
7	2091.4	89.3	2341	18	AAT75687
8	2091.4	89.3	2341	18	AAT75689

9	2089.8	89.3	2341	18	AAT75683	Mutant PB2 protein
10	2088.2	89.2	2341	18	AAT75684	Mutant PB2 protein
11	2088.2	89.2	2341	18	AAT75685	Mutant PB2 protein
12	1806.6	77.2	2341	22	AAD15674	Equine influenza v
13	1801.8	77.0	2341	22	AAD15675	Equine influenza v
14	964.2	41.2	1241	21	AAZ50977	Wild type equine i
15	964.2	41.2	1241	21	AAZ50978	Equine influenza v
16	962.6	41.1	1241	21	AAZ50978	Cold-adapted equin
17	962.6	41.1	1241	21	AAZ50978	Equine influenza v
18	941.4	40.2	1233	21	AAZ50979	Wild type equine i
19	941.4	40.2	1233	21	AAZ50979	Equine influenza v
20	938.2	40.1	1232	21	AAZ50981	Cold-adapted equin
21	938.2	40.1	1232	21	AAZ50981	Equine influenza v
22	382.8	16.4	2396	24	AAD37062	Influenza B virus/
23	107.8	4.6	162	15	AAQ74184	5' end fragment of
24	58.2	2.5	80	21	AAZ54302	Primer Pol1-5'/PB2
25	58.2	2.5	80	24	AAZ54302	RNA polymerase I c
26	49.4	2.1	67	21	AAZ54303	Primer Pol1-3'/PB2
27	49.4	2.1	67	24	AAZ54303	RNA polymerase I c
28	48.4	2.1	50	18	AAT75795	RNA fragment from
29	48.4	2.1	50	20	AAZ79180	Influenza virus PB
30	48.4	2.1	50	20	AAZ79180	Oligonucleotide se
31	44.6	1.9	60	21	AAZ63624	Influenza virus PB
32	44.6	1.9	60	24	ABK90902	Influenza virus A
33	44.6	1.9	60	24	ABK90902	PB2 tryptophan mod
34	42.4	1.8	6741	21	AAZ10595	Gene encoding a su
35	42.2	1.8	3579	21	AAZ10595	Plasmodium falcipa
36	41.6	1.8	14041	22	AAZ48029	Internal control B
37	39.8	1.7	10732	21	AAZ10594	Gene encoding a su
38	39.6	1.7	160755	23	AAZ88704	Human DNA sequence
39	38.8	1.7	2577	22	AAZ02134	Degenerate human a
40	38.6	1.6	1212	21	AAZ40218	Plasmodium falcipa
41	38	1.6	4590	22	AAZ4065	Yeast AOD9604-asso
42	37.2	1.6	1998	21	AAZ70212	Plasmodium falcipa
43	37.2	1.6	2277	19	AAZ13834	Homo sapiens ambig
44	37.2	1.6	2277	19	AAZ05370	Human telomerase p
45	37.2	1.6	5994	21	AAZ0222	Plasmodium falcipa

## ALIGNMENTS

RESULT 1	
AAD37054	
ID	AAD37054 standard; cDNA; 2341 BP.
XX	
XX	21-AUG-2002 (first entry)
XX	
XX	Influenza A virus/singapore/1/57/ca PB2 mutant cDNA.
DE	
XX	Attenuated influenza vaccine; prophylactic; therapeutic; infection;
XX	virus; gene; PB2 protein; mutant; ss.
KW	
OS	Influenza A virus.
OS	Synthetic.
XX	
XX	
FT	Key
FT	CDS
FT	
FT	Location/Qualifiers
FT	28..2340
FT	/*tag= a
FT	/product= "PB2 mutant protein"
FT	/transl_except= (pos:2305..2307, aa:Xaa)
FT	/transl_except= (pos:2311..2313, aa:Xaa)
FT	/transl_except= (pos:2320..2322, aa:Xaa)
FT	/note= "Xaa corresponds to an in-frame stop codon;"
FT	CDS does not include stop codon"
FT	/partial
FT	replace (252, A)
FT	/*tag= b
FT	replace (581, T)
FT	/*tag= c
FT	replace (1046, G)
FT	mutation

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FT      /+tag= d
XX      MO200224876-A2.
XX      28-MAR-2002.
XX      25-SEP-2001; 2001WO-EP11087.
XX      25-SEP-2000; 2000EP-0120896.
XX      (POLY-) POLYMER SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX      Kalinger H, Egorov A, Ferko B, Romanova J, Kalinger D,
XX      WPI: 2002-416282/44.
XX      P-PSDB; AAE23108.
XX      Manufacturing live vaccine, by infecting Vero cells with virus,
XX      combining cells with serum-free cell culture medium, incubating cells
XX      in presence of protease and nuclease, harvesting virus and preparing
XX      vaccine.
XX      Example 4; Page 38-39; 90pp; English.
XX      The present invention relates to a method for isolating viruses from
XX      various sources and for producing live attenuated influenza vaccines
XX      in a serum-free African green monkey kidney (Vero) cell culture under
XX      conditions where alterations in the surface antigens of the virus due
XX      to adaptive selection are minimised or prevented. The method is useful
XX      for the manufacture of whole-virus vaccine, preferably attenuated live
XX      vaccine. It is useful for prophylactic or therapeutic administration
XX      against viral infection, preferably influenza virus infections. The
XX      present sequence is Influenza A virus/singapore/1/57/cg (cold adapted)
XX      PB2 mutant cDNA. This sequence is used in the exemplification of the
XX      invention.
XX      Sequence 2341 BP; 798 A; 416 C; 585 G; 542 T; 0 other;
SQ      Query Match      98.6%; Score 2309; DB 24; Length 2341;
        Best Local Similarity 76.2%; Pred. No. 0;
        Matches 1784; Conservative 537; Mismatches 20; Indels 0; Gaps 0;
QY      1 AGCGAAGCAGGUCUAUUUAUUGAAGAAAGAAUAAAGAAUUAUUGAAGAAUUGAAG
DB      1 AGCGAAGCAGGUCUAUUUAUUGAAGAAAGAAUAAAGAAUUAUUGAAGAAUUGAAG
QY      61 UCGGAGUCUCCAGUCGCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      61 UCGGAGUCUCCAGUCGCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      121 AAGAAAGUACACUUCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
DB      121 AAGAAAGUACACUUCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY      181 GCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      181 GCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      240 GCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      240 GCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      300 GAGCAAGGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      300 GAGCAAGGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      360 UCACUUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCU
DB      360 UCACUUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCUUCGUCU
QY      420 CCAAAAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      420 CCAAAAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      480 CCUGUCCAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      480 CCUGUCCAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU

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QY      540 GCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      540 GCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      600 GUUGGGGGCGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      600 GUUGGGGGCGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      660 GAAUUCUCCAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      660 GAAUUCUCCAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      720 GUUCCGAAAAAGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
DB      720 GUUCCGAAAAAGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
QY      780 UUGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      780 UUGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      840 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      840 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      900 GUUCCAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      900 GUUCCAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      960 ACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      960 ACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      1020 AAGGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1020 AAGGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      1080 AGAAAGGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1080 AGAAAGGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      1140 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1140 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA
QY      1200 GCTATCTCAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG
DB      1200 GCTATCTCAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA
QY      1260 CAGUCGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1260 CAGUCGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      1320 AAGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1320 AAGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      1380 AAGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1380 AAGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      1440 GAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1440 GAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
QY      1500 GAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU
DB      1500 GAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU

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Key	Location/Qualifiers
QY	1561 CUAACAUCUCCUGAGAGAGUGUAGUAAAACAAGGGAACAAGAAAACUGAACUAUAAUCUAC 1650
Db	1561 CTACTATGCTCTGAGAGAGGTCACTGTAACACAGGGAAACAAGAAAACCTACAACTAACTTAC 1620
QY	1621 UCAUUGCUCAUAUGAUGUGGAGAGUUAUUGGCCCUAGUCAGUGUUGUGUUAUAUACUACUACAG 1680
Db	1621 TCATCGTCAATGATGTGGAGAGTTAAATGGCCCTGAGTGAAGTGTGGTCAATACCTATACAG 1680
QY	1681 UGGAUCAUCAGAAACUGGGAAAACUGUUAUAAAUAUUCUGUGGUCUCAGAAUCCUACAUGCUA 1740
Db	1681 TGGATCATACAGAAACUGGGAACCTGTAAAAATTCAGTGGTCTCAGAAATCTACAAATGCTA 1740
QY	1741 UACAAUAAAUAUGAAUUUUGAGCCAUUCUACUUCUACAAUAGAGAGAGUUAUUCUGGGACAUAUUGAU 1800
Db	1741 TACAAUAAAUAUGAAUUAUUGAGCAUUAUUGAGCAUUAUUGAGCAUUAUUGAGCAUUAUUGAGCA 1800
QY	1801 UACAGUGGUGUUGUUAAGGACUCUAUUCUACAAUAGAGAGAGUUAUUCUGGGACAUAUUGAU 1860
Db	1801 TAGAGTGGGTTTGTGAGAGCTCTAATTCUACAAUAGAGAGAGUUAUUCUGGGACAUAUUGAGCA 1860
QY	1861 ACCACCCAGAUAAUUAUAAAACUUCUUCUCCUUGCCUAGCCGCCGCCACCAAAAGUAUAGAUG 1920
Db	1861 ACCACCCAGATPAATPAACCTTCTTCCTTGGAGCCGCCGCCACCAAAAGUAUAGAUG 1920
QY	1921 CAGUUCUUCUACUCAUCUGUUAUUGUGAGGGGUAUCAGAAUAGAAUAUUAUUGUUAAGGGGC 1980
Db	1921 CAGTCTCTCTTCAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUA 1980
QY	1981 AAUUCUCCUUAUUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUAUUGAUA 2040
Db	1981 AATTCTCTCTGATTTCACTAACCAAGCACTTAAGAGACTTAACAAATTTCTGGAAAGGAT 2040
QY	2041 GCUGGACAUUUAACUGAAAGCCAGAUAGAAAGCAUUCUGGAGUGAGUCCGCUUUCUG 2100
Db	2041 CCGGACACTTAACTGAAGACCCAGATGAAGGACATCTGGAGTGGAGTCCGCTGTTCTG 2100
QY	2101 AGAGAUUCCUUAUUCUGGCAAAAGAGAUUAGAUUAGAUUAGCAUUAUAGCAUUAU 2160
Db	2101 AGAGATTTCTTCATTTCTTGGGCAAAAGAAATAGAGATATGCAACAGCAATTAAGCATCAAT 2160
QY	2161 GAACUGAGUAACUUGGCGAAAGAGAAAGGCUAUAUUGUAUUAUUGGGCAAGAGACGUG 2220
Db	2161 GAACUGAGUAACUUGGCGAAAGAGAAAGGCUAUAUUGUAUUAUUGGGCAAGAGACGUG 2220
QY	2221 GUGUUGUAUUGAAACGAAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACG 2280
Db	2221 GTGTTGGTAATGAAGAAAGAAAGGAGCTTACGACTACTACTGACACGACGACGACGACGACGACGACG 2280
QY	2281 AAAAGGAUUGCGAUGGCCAUCAUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUA 2340
Db	2281 AAAAGGAUUGCGAUGGCCAUCAUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUA 2340
QY	2341 U 2341
Db	2341 T 2341
RESULT 2	
ABA93934	standard; DNA; 2341 BP.
XX	ABA93934;
XX	07-MAY-2002 (first entry)
XX	Influenza A/Udorn/72 (H3N2) Strain PB2 encoding DNA SEQ ID NO.1.
XX	Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
XX	Influenza A virus; genome; gene; ds.
XX	Influenzavirus A.
XX	

FT	CDS		28..2307
FT		/tag=	a
FT		/product=	"PB2 protein"
PX			
PV			
XX	M0200200884-A2.		
XX			
PD	03-JUN-2002.		
PE	21-JUN-2001; 2001WO-US19826.		
PR	23-JUN-2000; 2000US-213650P.		
XX	(AMCY ) AMERICAN CYANAMID CO.		
PA	Galarza JM, Latham TE;		
P1	Galzarza JM, Latham TE;		
DR	WPI: 2002-139923/18.		
DR	P-PDB; ABB05764.		
PT	Polynucleotide encoding complete sequence of influenza A/Udorn/72 and variant strains -		
PS	Claim 1; Page 44-47; 103pp; English.		
XX	The present invention describes an isolated polynucleotide (I) having the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive strand, antigenomic message sense. ABA93934 to ABA93944 encode the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774 from the present invention. (I) is useful for designing polymerase chain reaction (PCR) primers for use in a PCR assay to detect the presence of the corresponding virus segment in a sample or for designing and selecting peptides for use in an enzyme linked immunosorbant assay to detect the presence of the corresponding protein produced by that segment in a sample, hence is useful in diagnosis and may be modified by mutation to generate new influenza A variant strains. ABA94945 to ABA94943 represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which are used in an example from the present invention.		
SQ	Sequence 2341 BP; 794 A; 419 C; 587 G; 541 T; 0 other;  Query Match            92.8%; Score 2173; DB 24; Length 2341; Best Local Similarity     73.3%; Pred. No. 0; Matches 1715; Conservative 521; Mismatches 105; Indels 0; Gaps 0		
OY	1 AGCGAAGACGAGUCAUUUUUAUCAUUGGAAGAUAUAAACAUCAGCAUCCUANG 60		
Db	1 AGCAAAGCAGGGTCAATTATTTTCATAVTGGAAAAAATTAAGAACCTACGC GAATCTGTATG 60		
OY	UGCACAGUCGCGACUCGCGAGAGUUAACA AAAACACACAGUGGCCAUUAGCCAUUAU 120		
Db	61 TCGCAGTCTCGACTTCGGGAAGTACTAACAAAACCACAGTGACCATATATTT 120		
OY	AAGAAGUACACUACGAGGAGCGACGAAAAAG ACCGCUACUUGAGUAGUAAUUGG AUGAU 180		
Db	121 AAGAAATCACATCAGTAGGAGACAGAAAAAG AACCCGTCACUTTAGAGATGAAATG ATGATG 180		
OY	181 GCACUAAAUUCCGUAUDUACGCGCAGCAAGAG UUAACAGAAUUGAUUCCUGAGAAU 240		
Db	181 GCATTAATAATATTCACAAATTACAGCTG ACACAAAGGAGTAAACA AAATVGTTCTCTGAG AAAAAAT 240		
OY	241 GAGCAAGGCGCAACUUCUUVUGAGUAA AUUGAGUGAGUCGCGGANUGGUGUGUGAUG UA 300		
Db	241 GAGCAAGGCGCAAAACCTATGGAGTRAAAT TGATGATATCCGAGTCCAGTCAAGATG GTA 300		
OY	301 UCACUCUUGCGUGUAGUUGUGAGUAUUGA AUAUGACCAUUGACAAGUACG GUUCUUAU 360		
Db	301 TCACCTTTGGCGGTGACATGGGTGAAT TAAGAAATGAGACCA GTGACCAAGTACCG TT CATTAAT 360		
OY	361 CCAAAAAUUACAAAUUUAUUUGAGAAAGUC CAAGGUUUAUACAUUGAGAAC CUUUGCC 420		
Db	361 CCAAAAGTCTACACACCTTAATTTGATTAAG CTCCAAGAGGTTTTAAACATGGA ACTTTGGC 420		

QY	421	CCUCGUCUUUUUAGAAACCAAGUCAAAUAUAGCGCCAGAGAGUUGACAUAUAUUCUCUGUACAU	480
Db	421	CTGTGCCATTTTAGAACCAGATCAAAATACCCCGAAGAGTTGACATTAACCTTGTCAT	480
QY	481	GCAGACCUACAGUGCCAGAGGCGACAGAGUUGUAUACUGAAAGUUGUUUCCUUAACGAA	540
Db	481	GCAGACCTCAAGTCCCAAGAGGCGACAGAGTGTAAATCAAGAAAGTTGTTTTCCCAATGAA	540
QY	541	GUGGGGGCGAGGAUUCUAACGUGCGGAUCCGCAUUAACAUAAACCAAGAGAAAAAGAA	600
Db	541	GTGGGGGCGCAGGATACTAAACGTGGAAATCAATTAACATTAACCAAGAGAAAAAGAA	600
QY	601	GAACUCCAGAGUUGGCAAAAUUUCACCUUUGAGUGUGUGUAACUGUUNAAGAGAAACUU	660
Db	601	GAACUCCAGAGATGCAAAATTTCTCTTTGATGGTTGCAATCATGTTAGAGAGAACTT	660
QY	661	GUCCGAAAAACGAGAUUUUUCUCCAGUUGUCUGUGGAGACAGACGUGUGUAUCAUUGAAGUG	720
Db	661	GTCCGAAAAACGAGATTTCTCCCAATGCTGTGTGAAACAGACAGTGTGTACATTTGAACTG	720
QY	721	UUGCACUUAGACUACAAGSAAACAUUGCUGGGGAAACAGUUGUACUCCGCGAGGAGAAUAGAG	780
Db	721	TTACCTTGACTCCAAAGAACGTGTTGGGAAACGATGTACCTCCAGGTGGAGAACTGAGG	780
QY	781	AUAGAUAGUUGUAUCAAAGUCUUAUUUUAUUGCAGCCAGAGCAAGUAAGUAGAAAGACAGCA	840
Db	781	AATGACGATGTTGACCAAAAGCCTTAATTAATGACGACAGAAACATAGTGAGAAAGACAGCA	840
QY	841	GUANUCAGACAUCCACUAGCAUCUUUAUUGAGAUUGUCCACAGACACACAUUUGGCGGG	900
Db	841	GTATCAGAGATCCACTGACCACTTTATTTAGAGATGTGCACAGACACTGATTTGGCGGG	900
QY	901	ACAAGSAGUGGAGCAUUCUUNUGGCGAGAAACCAACAGAAAGACAGCUGUGGAAUUAUAGC	960
Db	901	ACAAGSAGTGTGAGACATTTCTTAGCGAGAACCCGAGGAAAGAACAGCTGTGATATATGC	960
QY	961	AAGCUGCAUUGGCAUCUGAGAUACGUCUCCUACUUGUUUGCGGGUUCACAUUUAAG	1020
Db	961	AAGCUGTGAATGGGACTGAGAGATCAGCTCATCTTTCAGTTTGTGGGTTCACATTTAAG	1020
QY	1021	AGAACCAACGGGACUACUAGUCACAGAGAGAGAGAAAGUCUCUACCGGCAUUCUUAACA	1080
Db	1021	AGAACCAACGGGTCATCAATCAATCAAAAGAGAGAAAGTCTTAGCGGCAATTCCTAAACA	1080
QY	1081	UUGAAUAUAAGGUGUCACUGAGGGAUACGAGAGUUCACAUUGGUGGGAAAAAGGCAACA	1140
Db	1081	TTGAAAAATTAAGGCTCATGAGGGGTACGAGAGGTTTCAACAATGCTGGGAAAAAGGCAACA	1140
QY	1141	GCUAUAUCUACAAAAAGCAACCGAGAGAUUUGAUUCAGUCUUAUUGUAAGUUGAAACGAA	1200
Db	1141	GCTAATATCTACAAAAAGCAACCGAGAGATTTGCTTACGCTTAATGTAAGTGGAAAGGAGCAG	1200
QY	1201	CAGUCGAGAGCUGAGCAAAUAUUAUUGGCGCAGUGUAUUUUCACAGAAGAUUGUUAUGAU	1260
Db	1201	CAGTCAATATAGCCGAAGCCGATTAATGTAAGCATTGCTGTTTTCACAAAGAGATTGCATGATA	1260
QY	1261	AAAGCAGUAGAGUGAUCUGAUAUUUCGUUAUAGGCAUAUACGACGAUUGAUAUCCAG	1320
Db	1261	AAAGCAGTTAGAGGTGACCTGCAATTTTCGTTTAAACAGGCAAAATCAGCGGTGAATCCCATG	1320
QY	1321	CAUCAACUUUUAAGCAUUUUUCAGAAAGAGUUGGAAAAUUGUCUUUUUCAAUAUUGGGGAUU	1380
Db	1321	CATCAACTTTTAAAGCATTTTACAGAAAGATGCGAAAGTCTTTTTCAGATATTTGGGGAATT	1380
QY	1381	GAACAUUACGACAAUGUGAUGGGAUUGAUUGGGGUAUUUUCACAGACUAGCUCUACAAGACA	1440
Db	1381	GAACATATTCGACAATGTGATGTGGAAATGCTTGGAGTATTAACAGACATGACTCCMAAGACA	1440
QY	1441	GAGAUUGCAUUGAGAGGGGUAAAGAGUCACCAAAAUUGGGCGUAGUAGAAUAUUCUACAGCGG	1500
Db	1441	GAGATGTCAATAGAGGGAATAAGAGATCAGCAAAATGGGCGTGAATGAATATCTCCAGACA	1500

OY		1501	GAGGAGUUAUGGGUGACUUUAGCCCGGUUUUUUGAUUCUGACCAAGAGAUAUGA	1560
Db		1501	GAGGGGGATGTGGTTACGATTTCGGTTTTTGAAGATTGCAGACCCTAACTGGAAATGTA	1566
OY		1561	CUMCUAUCUCUCUGAGAGGUCAGUGAAAACAAGGGAAACAGNAAACUGAACUAUACUUC	1620
Db		1561	TTCATATCTCCTCGTAGGAGGTCAGTGAAACAACAGGGGACAGAGAGACTGACATAATCTTAC	1620
OY		1621	UCAUCGUAUAGUUGGGAGAUUAAVGGCCUGAGUICAGUGUGUGUUAUACCUAUUCAG	1680
Db		1621	TCATCGTCAATGATGTGGGAGATTAAATGGCCCTGAGTCAAGTGTGTCAATACCTATCAA	1680
OY		1681	UGGAGUVCUAGAAAACUGGAGAAACUGUGAAAAAUUCAGGUGUCUCAAUVCUCAAUUGCUA	1740
Db		1681	TGGATCATCTCGAATACTGGGAAACTGTTAAAAATTCATATGATCTCAGAAATGTTG	1740
OY		1741	UACAAUAAAAUUGGAUUUGAGGCCAUCUUCAGUCUUAUUGUCUUAAGGCCAUUAGAGCCAA	1800
Db		1741	TACACACAAAATGGAATTTGAGCCATTTCACTTATTTCTTAAGGCCATTAGAGGCCAA	1800
OY		1801	UACAGGGGUGUUGUUGAGACUCUUAUUCCAAACAAUAGAGGUAUGACUUGGGACAUUUGAU	1860
Db		1801	TACAGTGGATTTGTCAGAACTCTATTTCCAACAAATGAGGGAGTGTACTGGAGCAATTTGAT	1860
OY		1861	ACCACCCAGUAUAAAAACUUCUUCUUCUUGCACGCCCCCCCAACCAAGCAAAGUAGAUG	1920
Db		1861	ACCACCCAGATTAATMAAGCTTCTCCCTTTGGCACGCCCCCACCAAGCAAAGTATGAATG	1920
OY		1921	CAGUUCUCUCUACUGACUCUGUAAGUGUAGGGGAAUCAGAAUAGAGAUAUACUUGUAAAGGCG	1980
Db		1921	CAGTTCTCTTCTATTGACTGTGAATGTAGGGGATCAGGGATGAGAAATCTTGTAAAGGGCG	1980
OY		1981	AUUTCUCUUAUUVUCAAACUACCAACAGACCACUAAGACCUAACAUAUUCUCGAGAAAGAU	2040
Db		1981	AATTCCTCTGTATTCACCTACCAACAAGACCACTMAAAGACTMAACAATTCGAGAAAGAT	2040
OY		2041	GCUGGCAUCUUUAUCUGAAGACCCAGAUAGAGGCAUCUUCUGAGUGGAGUCCGCTUGUCUG	2100
Db		2041	GCTGGCACTTAAATTGAAGACCCAGATGAAAGCACATCCGGAGTGGAGTCCGCTGTTTTG	2100
OY		2101	AGAGGAAUUCUCUUAUUCUGGCGAAAGAAUAGUAGAGUAUUGGACCGCAACUVAAGCAUCAAU	2160
Db		2101	AGAGGATTTCTCATTTCTAGTTAGTAAAGAAATGAAAGATACGAGCCAGCATTTAAGCATCAAT	2160
OY		2161	GAAUCUGAUAACCUUGGAGAAAGAGAAAAAGGCUUAUUGUAGUAUUGGCGAAGAGACGUG	2220
Db		2161	GAACTGAGTAACTTTGCAAAAGAGAAAGGCTAATGTGCTAATTTGGGCAAGAGAACGTG	2220
OY		2221	GUGUUGGUUAUAGAAACAGAAACGGAACUCUAGCAUACUACUGACAGCCAGACACGCGACC	2280
Db		2221	GTTGTTGGTAATGAAACAGAAAACGGGAGCTCTAGCACTTACTTACGACAGCCAGACGCGACC	2280
OY		2281	AAAAAGAUUCGGAUUGGCGCAUCUAUUAUUGUUGAUAUGUTUAAAAAGCACCUUGUUUUAAC	2340
Db		2281	AAAAAGAAATTCCGATGGCCATCAATTAATGTTGAATAGTTTAAAAACGACCTTTGTTTAC	2340
OY		2341 U 2341		
Db		2341 T 2341		
<hr/>				
RESULT 3				
AAK82192 standard; DNA; 2341 BP.				
<hr/>				
XX	AAK82192;			
AC	18-AUG-1999 (first entry)			
DT	Influenza virus PB2 protein gene sequence.			
XX				
DE				
XX				
KW	Cold-adapted influenza virus; passage culture; PB2 protein; PB1 protein; PA protein; NP protein; M protein; NS protein; temperature sensitivity;			

[illegible]

[illegible]

	Mutant PB2 protein, ALA6, coding sequence.
KW	Influenza virus; PB2 protein; charged cluster; master donor virus;
KM	Influenza A virus A/LN/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KV	ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;
KW	vaccine; influenza virus A/Memphis/8/88; ss.
XX	
OS	Influenza virus.
XS	Synthetic.
XH	
FH	Key Location/Qualifiers
FT	CDS .2..2307
FT	/tag= a
FT	/product= ALA6
FN	
XX	
PD	12-DEC-1996.
PF	03-JUN-1996; 96MO-US08441.
PX	
PR	05-JUN-1995; 95US-0462388.
PX	(AVIR-) AVIRON.
PA	
PI	Coelingh KL, Parkin NT;
PX	
DR	WPJ; 1997-042859/04.
DR	P-PSDB; NAM07710.
PX	
PT	Recombinant influenza virus with mutation(s) in charged cluster regions - esp. temperature-sensitive mutation(s), has attenuated phenotype suitable in vaccines for preventing influenza
PT	
PS	Claim 7; Page -: 39pp; English.
XX	
CC	The sequences given in T75683-90 encode modified influenza virus PB2 proteins, ALA1-LA8. The modified proteins are generated by replacing certain Arg, Lys and Asp residues in one of 8 charged clusters CC identified in Influenza A virus A/LN/2/87 PB2 protein, with Ala
CC	residues. Specifically, the mutations are as follows: ALA1 (residues 2-6) ERIKE --> EAIAE, ALA2 (residues 120-124) DKVER --> DAVEA, ALA3 (residues 140-144) KIRRR --> KIAAA, ALA4 (residues 187-192) KEKKE --> KEAAEE, ALA5 (residues 339-343) KRREE --> KAEEE, ALA6 (residues 677-681)
CC	EEDPE --> EAPAA, ALA7 (residues 699-703) KEDRR --> KEDAA and ALA8 (residues 736-740) KKRD --> ARKRQ. Recombinant influenza viruses which contain these mutations produce attenuated viral phenotypes, useful as master donor viruses in the preparation of immunogenic compositions,
CC	e.g. vaccines, for preventing influenza, or a disease associated with influenza infection. Modification of charged cluster results with in consistent and predictable exhibition of temperature sensitivity.
CC	These sequences are not given in the specification and are based on the Influenza virus A/Memphis/8/88 given in Genbank M73517.
SO	
	Sequence 2341 BP; 802 A; 428 C; 575 G; 536 T; 0 other:
Query Match	89.5%; Score 2094.6; DB 18; Length 2341;
Best Local Similarity	71.7%; Pred. No. 0;
Matches 1678; Conservative 509; Mismatches 154; Indels 0; Gaps 0	
OY	1 AGCGAACACGAGUCUUAUUUUGCAAUAGAUAUAAAACAUCACGAUUCUGAUNG 60   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   Dy 1 AGCAAAACAGAGTCATTATTTCTTGGTGAAAAAGATAAAAAGACTACGAAACCCTGANG 60
Dd	61 UGCAGUCUCGCCAGCUCGCCAGAUUNCUAAACAAAACACAGUGGACCCAUAUGC 120   :  :    :    :    :    :    :    :    :    :    :    : Db 61 TC GGAGTCTCGGAGCTCCGGAATTAACA AAAAACACAGGTGAGCATATGCCCCATTAATT 120
OY	121 MAGAGUACACAUCCAGGAGCAGAAAGAACC CGGUACCUUAGAUAGAAUUGUGAUG 180   ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  : Db 121 MA GAAGTACACATCTAGGAGAGACAG AAAGAAACCCGTCACTTAGATTAAGATGAGTGAIG 180
OY	181 GCANUGAUAUUCG AUUACAGCCGACAAAGAGAUACAGAAUAGAUUUCUGAGAGAAU 240

Db 181 GCATGAAATATCAATCACTGACAAAAGATACAGAAATGTTCCGGAGAAAT 240  
 Qy 241 GAGCAGGGCAAACUUAUGAGUAUUAUGAGUCCCGAGUCCGUGUGAGUGUA 300  
 Db 241 GAAACAGGACAAACTATGAGATGAAATGATGATCTGGGTCAAGATGATGTA 300  
 Qy 301 UCAACUUGGUGUGAGUAGUAUUAUGAACCAUAGCAAGUACGUGUUAUUA 360  
 Db 301 TCACCCTTGCGAGACATGCTGGAATGAAATGACACAGTGCMAATAGGTTCACTAT 360  
 Qy 361 CCAAAAACUUAACUUAUUUUUAGAGAAAGUCGAAAAGUUAAAAUAGUAGCCUUGG 420  
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 Qy 421 CCUGUCCAUUUUAGAAACCAAGUCAAUAUACCGGAAGAGUGUACAUAUUAUCCUGUCAU 480  
 Db 421 CCTGTCCATTTTGAATAATCAAGTCAAAATAGCCGAAAGATGACATTAACCTTGGTCAAT 480  
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 Db 481 GCAGACCTCAGTGCAGAGAGGACCAAGATGTAAATTATGAGAGTTTCCCAATGAA 540  
 Qy 541 GUGGGGSCCAGAGUAUAAGUGCGAUAUUGCAAUUAACAUAUACCAAGAGAAAAAGAA 600  
 Db 541 GTGGAGCCAGAGATCTACATCAAGATCACAATTAACAATTAACCAAGAGAAAAAGAA 600  
 Qy 601 GAAACUCCAGAGUUGCAAAAUUUAACCUUUAUGUGUGUAGUAGUAGAGAGAAACU 660  
 Db 601 GAACTCCGAGATTCGAAATTTCTCTTGTATGTTGATCATATGTTAGAGAGAACTT 660  
 Qy 661 GUGCGAAAACGAGAUUUUCCCAAGUGUGUGAGAAACAAGCGUGUGUAUUGAAAGUG 720  
 Db 661 GTCCGAAAACGAGATTTCTCCAGTTGCTGTGGAAACAAGCAGTATATACATTTGAAGTT 720  
 Qy 721 UUCGACUUGACUUAACUAGCUGGGAACAGAGUUAACUACUCCAGUGAGAGAGAGAG 780  
 Db 721 TTACATTTGACTAGAGAACGTTGTGGAAACAATATGATACCTCAGGTGAGAGAGAGAG 780  
 Qy 781 AUAUGAUGAUGUAGUUAACUUAUUAUUGCAAGCCAGAGACUAGUGAGAGAGAGAGCA 840  
 Db 781 AATGACGATGTTGACCAAGACCTTAATTAATTGACAGCCAGAAACATATGAGAAAGAGCCGA 840  
 Qy 841 GUUUCACGACAUUACUAGACUUCUUAUUGGAGAGUGCCACGACACAGAUUGCGCG 900  
 Db 841 GTATCAGCAGATCAGCTAGCATCTTATTAAGATGTGCGACAGCACAAATTTGCGCGG 900  
 Qy 901 ACAAGAGUUGGAGACUUAAGCAGACCCCAACGAGAGAGACUUGGAGAAAUUAGC 960  
 Db 901 ACAAGAGTGGTGAACATTTCTTAGGACAGAACCCGACGAGAGAACAGCTGTGATATATGC 960  
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 Db 1081 TTAAAAATTAAGAGTGAAGTGAAGGAGTACAGAGAGTTCAATAGTGGGAAAAAGGCAACA 1140  
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Db 1261 AAAGCAGUUGAGUGUAGUUAUUGCUUAUUAUAGGCAAUUAGGAGUAGUUAUCCCAUG 1320  
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 Db 1741 TACAAUUAUUAUUGAAUUAUUGAACCAUUAUUGUUAUUGUUAUUGUUAUUGUUAU 1800  
 Qy 1801 UACAGUGGUGUUAUUGAGACUUAUUAUUGCAAAUUAUUGAGAGAGUUAUUGUUAU 1860  
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 Qy 1861 ACCACCCAGUUAUUAUUAUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUA 1920  
 Db 1861 ACCACCCAGUUAUUAUUAUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUA 1920  
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 Db 1921 CAGTCTCTCTATTTGACGTGAATGTGAGGAGATCAGGAGATGAATAATCTGTAAAGG 1980  
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 Qy 2341 U 2341  
 Db 2341 T 2341

RESULT 5  
AAT75690  
ID AAT75690 standard; cDNA; 2341 BP.  
XX  
AC AAT75690;  
XX  
DT 11-SEP-1997 (first entry)  
XX  
DE Mutant PB2 protein, ALA8, coding sequence.  
XX  
KW Influenza virus; PB2 protein; charged cluster; master donor virus;  
KW Influenza A virus A/LA/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;  
KW ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;  
KW vaccine; Influenza virus A/Memphis/8/88; ss.  
XX  
OS Influenza virus.  
OS Synthetic.  
Key Location/Qualifiers  
F- CDS 28..2307  
FT /tag= a  
FT /product= ALA8  
XX MO9639179-A1.  
XX 12-DEC-1996.  
XX 03-JUN-1996; 96WO-US08441.  
XX 05-JUN-1995; 95US-0462388.  
XX (AVIR-) AVIRON.  
XX Coeligh KL, Parkin NT;  
XX WPI; 1997-042859/04.  
XX P-PSDB; AAM07712.  
XX Recombinant influenza virus with mutation(s) in charged cluster  
XX regions - esp. temperature-sensitive mutation(s), has attenuated  
XX phenotype suitable in vaccines for preventing influenza  
XX  
XX Claim 7; Page -: 39pp; English.  
XX The sequences given in T75683-90 encode modified influenza virus PB2  
XX proteins, ALA1-ALA8. The modified proteins are generated by replacing  
XX certain Arg, Lys and Asp residues in one of 8 charged clusters  
XX identified in influenza A virus A/LA/2/87 PB2 protein, with Ala  
XX residues. Specifically, the mutations are as follows: ALA1 (residues  
XX 2-6) BIRK -> EATAR, ALA2 (residues 120-124) DYER -> DAVEA, ALA3  
XX (residues 140-144) KIRRR -> KIRAA, ALA4 (residues 187-197) KKKKE ->  
XX KEAEE, ALA5 (residues 339-343) KREBE -> AAREE, ALA6 (residues 677-681)  
XX EDPOE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8  
XX (residues 736-740) KKKRD -> ARKKD. Recombinant influenza viruses which  
XX contain these mutations produce attenuated viral phenotypes, useful as  
XX master donor viruses in the preparation of immunogenic compositions,  
XX e.g. vaccines, for preventing influenza, or a disease associated with  
XX influenza infection. Modification of charged cluster residues results  
XX in consistent and predictable exhibition of temperature sensitivity.  
XX These sequences are not given in the specification and are based on the  
XX influenza virus A/Memphis/8/88 given in Genbank M73517.  
XX  
SQ Sequence 2341 BP; 803 A; 426 C; 576 G; 536 T; 0 other;

Query Match 89.4%; Score 2093; DB 18; Length 2341;  
Best Local Similarity 71.6%; Pred. No. 0;  
Matches 1677; Conservative 509; Mismatches 155; Indels 0; Gaps 0;

1 AGCGAAGCAGGUCUAUUUAUUGCAUUAUUGCAUUAUUGCAUUGCAUUGCAUUG 60  
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61 UCGCAGUCUCGCACTUCGCGAGUACUAAACCAAAACCAAGUGACCAUUGGCCUAAU 120  
61 TCGCAGTCTCGCACTCGCGAGATACAAACCAAAACCAAGTGCACATATGGCCATAAT 120  
121 AAGAAGUACAUUCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
121 AAGAAGTACCAUCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
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421 CCGTCATTTTGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 480  
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481 GCAGACCTCAGTGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
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961 AAGCUGCAUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
961 AAGGCTGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
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1021 AGAACAAGCGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080  
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1081 TTGAAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140



```

Qy 1141 GCUAUAUCACAGAAAAGCAACGAGAGAUUGUACGUGAUUGUGAGGAAAGACGAA 1200
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Qy 1621 UCAUGUCUAUAGUAGUGGAGAUUAUUGCCUGAGUCAGUGUGUGUUAUUCUA 1680
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1621 TCATCCCTCATGTATGTGAGGATTAACGCGCTGAGTCCGTGTGCTAATCTAT 1680
Qy 1681 UGGAUCUAUGAGAAACUGGAGAAACUGUUAUAUUCAGUGUUCUACAUUCUA 1740
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1681 TGGATCATCAGAAATGAGGAAATGTTAAATTCATTAATGCTTCAGAAATCT 1740
Qy 1741 UACAAUAAAUAGGAAUUGGACAUUUCAGUCUUAUUGGAGGAGGAGGAGGCA 1800
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1741 TACAACAAATGGAATTTGACATTTCACTTTAGTTCTTAAGGCCATTAAGAG 1800
Qy 1801 UACAGUGGUGUUGUUGAGACUCUUAUUCACAAAUAGAGGAGUAGUACAU 1860
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1801 TACAGTGAATTTGTGAGAACTGATTCACAAATGAGAGATGCTTGAGCA 1860
Qy 1861 ACCACCCAGAAUUAUAAACUUCUCCUUGCAGCCGCCACCAAGGAAAGUA 1920
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1861 ACCACCCAGATATTAAGCTTCTCCCTTTTTCAGCGCTTCACCAAGGAAAG 1920
Qy 1921 CAGUUCUCUUCACUGACUGUGAAGUGAGGAGGAGUAGAAUAGGAGGAGG 1980
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1921 CAGTTCCTCTCATGTGATGTGAATGTGAGAGGAGTCAAGATTAATCTT 1980
Qy 1981 AAUUCUCUUAUUAUUAACUACACAGACACAUAGAGACUUAUUCUGGAAAG 2040
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1981 AATTCCTCTGTATTAACCTACCAAGACACCTTAAGAGCTTAACATTCGGA 2040
Qy 2041 GUGGACAUUAUACUGAGACCCAGAUAGAGCAUUCUGAGUGGAGUGCCUG 2100
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2041 GCTGACACTTTAATGAGAGACCCAGATGAAACACACTCCGAGTGCCTCT 2100
Qy 2101 AGAGAUUCUCUACUUCUGGAGAAAGAGUAGAGAUUGAGCCAGAUUAAG 2160
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2101 AAGAGATTTCTCATTTAGTAAAGAGACAGAAAGTACGAGCAGCATTAAG 2160
Qy 2161 GAAUGAGUAAACCUUGCGAAGAGAGAAAGGCUUAUUGUAGGAGAGAGAG 2220
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2161 GAACTAGTAACCTTGCAAAAGAGGAGAAAGGCTAATGTCTAATTTGGGAGAGAG 2220
Qy 2221 GUGUUGUUAUUAAGAACGAAACGGAACUCUAGCAUAUCUACAGCAGCAG 2280

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Db 2221 GTGTTGTAATGCGCAGAAAAACGAGACTCTTGCAATCTTACTGACAGCCAGACGAC 2280
Qy 2281 AAAAGAUUCGAGUGGCGCAUUAUUGUUAUAGUUAUUAUUAUUAUUAUUA 2340
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2281 AAAAGAAATTCGAGGCGCATCAATTAATGTTGAATAGTTTAAAAACGACT 2340
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 2341 U 2341
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2341 T 2341

RESULT 6
AAT75686
ID AAT75686 standard; cDNA; 2341 BP.
XX
AC AAT75686;
XX
DT 11-SEP-1997 (first entry)
XX
DE Mutant PB2 protein, ALA4, coding sequence.
XX
KW Influenza virus; PB2 protein; charged cluster; master donor virus;
KW Influenza A virus A/LA/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KW ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;
KW vaccine; Influenza virus A/Memphis/8/88; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 28..2307
FT /tag= a
FT /product= ALA4
PM M09639179-A1.
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US08441.
XX
PR 05-JUN-1995; 95US-0462386.
XX
PA (AVIR-) AVIRON.
PI Coelighh KL, Parkin NT;
XX
DR WPI: 1997-042859/04.
DR P-PSDB: AAM07708.
XX
PT Recombinant influenza virus with mutation(s) in charged cluster
PT Regions - esp. temperature-sensitive mutation(s), has attenuated
PT phenotype suitable in vaccines for preventing influenza
XX
PS Claim 7; Page -: 39pp; English.
XX
CC The sequences given in T75683-90 encode modified influenza virus PB2
CC proteins, ALA1-ALA8. The modified proteins are generated by replacing
CC certain Arg, Lys and Asp residues in one of 8 charged clusters
CC identified in influenza A virus A/LA/2/87 PB2 protein, with Ala
CC residues. Specifically, the mutations are as follows: ALA1 (residues
CC 2-6) BRIKE -> EAIAG, ALA2 (residues 120-124) DKVER -> DAVEA, ALA3
CC (residues 140-144) KIRRR -> KIIAA, ALA4 (residues 187-192) KEKKEE ->
CC KEAAEE, ALA5 (residues 339-343) KREBE -> AAEEF, ALA6 (residues 677-681)
CC EDDEE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8
CC (residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which
CC contain these mutations produce attenuated viral phenotypes, useful as
CC master donor viruses in the preparation of immunogenic compositions,
CC e.g. vaccines, for preventing influenza, or a disease associated with
CC influenza infection. Modification of charged cluster residues results
CC in consistent and predictable exhibition of temperature sensitivity.
CC These sequences are not given in the specification and are based on the
CC Influenza virus A/Memphis/8/88 given in Genbank M73517.

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XX Sequence 2341 BP; 800 A; 427 C; 577 G; 537 T; 0 other;

89.3%; Score 2091.4; DB 18; Length 2341;

Query Match Best Local Similarity 71.6%; Pred. No. 0; Mismatches 156; Indels 0; Gaps 0;

Matches 1676; Conservative 509; Mismatches 156; Indels 0; Gaps 0;

QY 1 AGCGAAGACAGGUCUAUUUAUUCUAUUGAAGAAUAAAAGAAACUACCGAAUUCUGAUG 60  
 DB 1 AGCGAAGACAGGUCUAUUUAUUCUAUUGAAGAAUAAAAGAAACUACCGAAUUCUGAUG 60  
 QY 61 UCGGAGUUCUGCAUUCGCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120  
 DB 61 UCGGAGUUCUGCAUUCGCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120  
 QY 121 AAGAAAGACACAUACGAGGAGGACAGAAAGAAACCCGACUAGGAGUAGAAUUGAUGAUG 180  
 DB 121 AAGAAAGACACAUACGAGGAGGACAGAAAGAAACCCGACUAGGAGUAGAAUUGAUGAUG 180  
 QY 181 GCAUAGAAUUAUUCGAAUUAACAGCCGACAAAGAGAUAAACAGAAUUGAUUUCUGAGAAAU 240  
 DB 181 GCAUAGAAUUAUUCGAAUUAACAGCCGACAAAGAGAUAAACAGAAUUGAUUUCUGAGAAAU 240  
 QY 241 GAGCAAGGCAAAUCUUAUUGAGUAUUAUUGAUGUACCGGAGUUGGAGUUCGUGAGUA 300  
 DB 241 GAGCAAGGCAAAUCUUAUUGAGUAUUAUUGAUGUACCGGAGUUGGAGUUCGUGAGUA 300  
 QY 301 UACACUCUGGUGUAGUUGGAGUAUUAUUGAAGAAUUGAAGAAUUGAAGAAUUGAAGAAU 360  
 DB 301 UACACUCUGGUGUAGUUGGAGUAUUAUUGAAGAAUUGAAGAAUUGAAGAAUUGAAGAAU 360  
 QY 361 CCAAAAAUCUACAAACUUAUUUUGAAGAAUUGAAGAAUUGAAGAAUUGAAGAAUUGAAG 420  
 DB 361 CCAAAAAUCUACAAACUUAUUUUGAAGAAUUGAAGAAUUGAAGAAUUGAAGAAUUGAAG 420  
 QY 421 CCUGUCCAUUUUUAAGAAACCAAGUCAAUUAUUGCCGAGAGUUGGUAUUAUUCUGUACU 480  
 DB 421 CCUGUCCAUUUUUAAGAAACCAAGUCAAUUAUUGCCGAGAGUUGGUAUUAUUCUGUACU 480  
 QY 481 GCAGACUCUAGUUGCAAGAGAGGACAGAGUUAUUAUUGAAGAAUUGAAGAAUUGAAGAA 540  
 DB 481 GCAGACUCUAGUUGCAAGAGAGGACAGAGUUAUUAUUGAAGAAUUGAAGAAUUGAAGAA 540  
 QY 541 GUGGAGGACAGAGUAUUAUUGGAGAAUUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUA 600  
 DB 541 GUGGAGGACAGAGUAUUAUUGGAGAAUUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUA 600  
 QY 601 GAACUCUAGUUGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660  
 DB 601 GAACUCUAGUUGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660  
 QY 661 GUCCGAAAAAGAGAUUUUUCGAGUUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 720  
 DB 661 GUCCGAAAAAGAGAUUUUUCGAGUUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 720  
 QY 721 UUGCAUUGACUUAAGAAACUAGCUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 780  
 DB 721 UUGCAUUGACUUAAGAAACUAGCUGGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 780  
 QY 781 AAUGAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 DB 781 AAUGAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 QY 841 GUAUACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900  
 DB 841 GUAUACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 900  
 QY 901 ACAAGAGUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 DB 901 ACAAGAGUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 QY 961 AAGGUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020  
 DB 961 AAGGUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020

DB 961 AAGGUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1020  
 QY 1021 AAGACAAAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080  
 DB 1021 AAGACAAAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1080  
 QY 1081 UUGAAAUUAAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1140  
 DB 1081 UUGAAAUUAAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1140  
 QY 1141 GCUAUAUCAGAAAGAAACAGAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1200  
 DB 1141 GCUAUAUCAGAAAGAAACAGAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1200  
 QY 1201 CAGUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1260  
 DB 1201 CAGUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1260  
 QY 1261 AAGGAGUUAAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1320  
 DB 1261 AAGGAGUUAAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1320  
 QY 1321 CAUCAAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1380  
 DB 1321 CAUCAAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1380  
 QY 1381 GAACAUUAUUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1440  
 DB 1381 GAACAUUAUUGCAUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1440  
 QY 1441 GAGAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1500  
 DB 1441 GAGAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1500  
 QY 1501 GAGAGUUAAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1560  
 DB 1501 GAGAGUUAAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1560  
 QY 1561 CUACUUAUCUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1620  
 DB 1561 CUACUUAUCUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1620  
 QY 1621 UCAUUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1680  
 DB 1621 UCAUUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1680  
 QY 1681 UGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1740  
 DB 1681 UGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1740  
 QY 1741 UACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1800  
 DB 1741 UACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1800  
 QY 1801 UACAGUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1860  
 DB 1801 UACAGUUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1860  
 QY 1861 ACCAGCAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1920  
 DB 1861 ACCAGCAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1920  
 QY 1921 CAGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1980  
 DB 1921 CAGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1980  
 QY 1981 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2040  
 DB 1981 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2040  
 QY 2041 GUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2100  
 DB 2041 GUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2100



OY		2101	AGAGAAGUUCUUAUUUGGCGAAAAGAGUAGAGAUUUUGACCGAGUUAAAGCAUUCAU	2160
Dd		2101	AGAGAATTTCATTTCTAAGTGAAGAGACAGAAAGTAACGGACACGACTTAAGCATTCAT	2160
OY		2161	GAACTGAGTAACCTTGCCAAAAAGGGGAAAAAGCGTTAATGTGCTAATTGGGCCAAGAGACCTG	2220
Dd		2221	GUGTGTGTAATTATAAAGCAAAAACGGGACTCTTACGATTACTTAAGACGCAGACGCGACC	2280
OY		2281	AAAAGAUUCGGAGUUGGCCCAUCAUUUAUGUGUAGUAUUUUAAAACGACCTUUGUUCAC	2340
Dd		2281	AAAAGAUUCGGAGUUGGCCCAUCAUUUAUGUGUAGUAUUUUAAAACGACCTUUGUUCAC	2340
OY		2341	U 2341	
Dd		2341	T 2341	
OY		2341	T 2341	
RESULT 7				
ID	AAT75687			
XX	AAT75687	standard; cDNA; 2341 BP.		
XX	AAT75687;			
DT	11-SEP-1997	(first entry)		
DE	Mutant PB2 protein, ALA5, coding sequence.			
KM	Influenza virus; PB2 protein; charged cluster; master donor virus;			
KM	influenza A virus A/LA/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;			
KM	ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;			
KM	vaccine; influenza virus A/Memphis/8/88; ss.			
OS	Influenza virus.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	CDS	28..2307		
FT		/tag= a		
PN		/product= ALA5		
XX	MO9639179-A1.			
XX	12-DEC-1996.			
XX	03-JUN-1996;	96MO-US08441.		
PR	05-JUN-1995;	95US-0462380.		
PA	(AVIR-) AVIRON.			
PI	Coeltingh KL; Parkin NT;			
DR	WPI; 1997-042859/04.			
DR	P-PSDB; AAM07709.			
PT	Recombinant influenza virus with mutation(s) in charged cluster			
PT	regions - esp. temperature-sensitive mutation(s), has attenuated			
PT	phenotype suitable in vaccines for preventing influenza			
PS	Claim 7; Page -: 39pp; English.			
CC	The sequences given in T75683-90 encode modified influenza virus PB2			
CC	proteins, ALA1-ALA8. The modified proteins are generated by replacing			
CC	certain Arg, Lys and Asp residues in one of 8 charged clusters			
CC	identified in influenza A virus A/LA/2/87 PB2 protein, with Ala			
CC	residues. Specifically, the mutations are as follows: ALA1 (residues			
CC	2-6) ERIKE -> EARAE; ALA2 (residues 120-124) DVER -> DAVEA; ALA3			
CC	(residues 140-144) KIRR -> KIAAA; ALA4 (residues 187-192) KEKKEE ->			

CC KEAAEE, ALA5 (residues 339-343) KREEE -> AAEEE, ALA6 (residues 677-681)  
CC EDPEE -> EAPAA, ALA7 (residues 699-703) KEPRR -> KEEDA and ALA8  
CC (residues 736-740) KRKKD -> AKKKD. Recombinant influenza viruses which  
CC contain these mutations produce attenuated viral phenotypes, useful as  
CC master donor viruses in the preparation of immunogenic compositions,  
CC e.g. vaccines, for preventing influenza, or a disease associated with  
CC influenza infection. Modification of charged cluster residues results  
CC in consistent and predictable exhibition of temperature sensitivity.  
CC These sequences are not given in the specification and are based on the  
CC influenza virus A/Memphis/8/88 given in Genbank M73517.  
XX  
XX Sequence 2341 BP; 801 A; 427 C; 576 G; 537 T; 0 other;

Query Match	Similarity	89.3%	Score 2091.4	DB 18	Length 2341
Best Local	71.6%	Pred. No. 0			
Matches 1676	Conservative 509	Mismatches 156	Indels 0	Gaps 0	
QY	1	AGCGAAACGACGUCAUUUUAUUCGAAUUGGAAAGAAUAAAAGAAACUAACGGAUUCUGAUG	60		
Db	1	AGCAAAAGCAGGTCAATTATATTTTCAGTATGGAAGAAATAAAAAGAACTACGGAACCTGATG	60		
QY	61	UCCGAGUCUCCGACUCCGCGAGAUUCAAACAAAACCAAGUGGACCAUUGGCCUAUAUUG	120		
Db	61	TGCGAGCTCTCCCACTCGGAGATACTAAACAAAAACCAAGTGGACCAATATGCCCTAAATT	120		
QY	121	AGAAGUACAUCCAGGGGACGAGAAAAAGAACCCGUCACUUGAGUAAAAUUGAUGAUG	180		
Db	121	AAAGAAATCAATCAAGGAGACAGAAAAAGAACCCGTCACCTTAGATGAATGAAATGATGATG	180		
QY	181	GCAUUGAAUUAUCCGUAUACAGCCGACAAAGAUAAACAGAAUUGAUUUCUGAGAGAAU	240		
Db	181	GCAATGAAATTCCAATCACTGCTGACAAAAGATTAACAGAAATGGCTCCGAGAGAAAT	240		
QY	241	GAGAGAGGCGAAACUCUAUUGGAGUAAAAUGGUGAUGCCGAAUGCGAUGUGUGUA	300		
Db	241	GAACAGAGCAAACTCTATGGAGTAAATGTAGTGTGGGTGTCAGATCGAGTGTATGTA	300		
QY	301	UCACUCUGCGCUGUACUGUGUGAAUUGAAUUGGACCAUAGCAAGUACGGUUCUAUUAU	360		
Db	301	TCACCTCTGGCAGTGAACATGGTGAATGAAATGGAACGATGACAAATACGTTCACTAT	360		
QY	361	CCAAAAUUCUACAAAACUUAUUUUGAGAAAAGUCGAAAGGUAUAAAACATGAAACCUUUGGC	420		
Db	361	CCAAAAGCTACAAAGACTTATTTTGAACAAATCGAAAGTTTAAACATGGAACCTTTGGCC	420		
QY	421	CCUGUCAUUUUAAGAAACCAAAGUCAAUAUAGCGCGGAAGAGUGACAUUAUUCUGGUCAU	480		
Db	421	CCCTGCTCATTTTAAAGATCAAGTCAAAATACGCCGAAGATGACATTAACCTCGTCAAT	480		
QY	481	GCAGACCUCAUGUCGCAAGAGAGCAACAGAUUGAAUUAUGAAGUUGUUCUCCUAAACGA	540		
Db	481	GCAACCTCAAGTGCCAAAGAGGCAACAGATGTAATTTGGAAGTTGTTTTCCCAATGAA	540		
QY	541	GUGGGGGCCAGAAUACUAAACGUCGAAUUGCAUUAACAAUAAACAAAGAAAAAAGAA	600		
Db	541	GTTGGAGCCAGATATCTACATTCAGAAATCAAAATTAACAAATTAACCAAGAAAAAGAA	600		
QY	601	GAACUCCAGAUUUCGAAAUUUCACACUUGAGUGUGUACUUGAUGUAGAGAGAAACUU	660		
Db	601	GAATCTCGAGATTGCAAAATTTCTCTTTGATGGTTGCAATCAATGTTAAGAGAGAACTT	660		
QY	661	GUCCGAAAAAACGAGAUUUCUCCGAGUUGCUGGUGGAAACAGCAGUGUUCACUUGAUG	720		
Db	661	GTCGAAAAACGAAATTTCTCCCAAGTTGCTGTGTGAACAAACAGATATATTAACATTGAATTT	720		
QY	721	UUCGACUUGACUCAGAGAAACUGGUGGGAACAGAAUGUACUCCACAGUGGAGAAAGUGAG	780		
Db	721	TTAATATTGACTCAAGGAACTGTTTGGGAACAAATGTATCACTCCAGGTGGAAGAACTGAG	780		
QY	781	AAUGAUGAUGUUGAUCAAAGUCUAUUAUUGCAGCCAGAGACUAUGAGAAAGACACGA	840		
Db	781	AATACGATGTGTGACAAAGCCTTAATTAATTCACCCAGGAAACATATGTGAGAAAGGCCCA	840		







QY	541	GUUGGGGCGGAGUAUCUAAAGUCGGAUUCGCAUUAACAUAACCAAGAGAAAAAGAA	600
Db	541	GTGGAGCCGAGGATACATMACTGACGAATCACAATTAAACAATAACCAAAAGAGAAAAAGAA	600
QY	601	GAACUCCAGGAGUUGCAAAAUUUCACCUUUAUUGUGUGUGUAUUGUUAAGAGAGAAACUU	660
Db	601	GAATCTCGAGATTGCAAAATTTCTCCCTTAAATGGTGGCAATCAATGTTAAGAGAGAACTT	660
QY	661	GUCCGAAAAACGAGAUUUCUCCAGUGUCGUGGAAACAAGAGUGUUAUCUUGAAUGU	720
Db	661	GTCCGAAAAACGAGATTTCTCCAGTTGGCTGGTGGAAACAGACAGTATATCAATTGAAGTT	720
QY	721	UUGCAUCUGACUACAAGAACAUUCUCUGGAAACAGAUUGACUUCACAGUGGAGAAUGUAG	780
Db	721	TTTACATTTGACTCAAGGAAAGTGTGGGAAACAATGTACACTCAGGTGGAGAAAGTGAAG	780
QY	781	AATGAGAUUUGUUAUCAAAGCUAAUUAUUGCAAGCCAGAGCAUUAUUGAGAAAGACACA	840
Db	781	AATGAGAGATTTTAAACCAAAAGCTTAATTTATGACCGAGAAACATATGTAGAAAGCCGGA	840
QY	841	GUUACGAGAUUCACUAGACUUCUUUAUUGAGAUUGGACACAGACACAGAUUGGACGG	900
Db	841	GTATCAGACGATCCATAGATCTTTATTAAGATATGGCAACAGACACAAATTTGGCGGG	900
QY	901	ACAAAGAUUGUGGACAUUCUUAUGGCAAAACCAACAGAAAGCAAGCTUGGAGAAAUUUC	960
Db	901	ACAAAGATGTGTGACATTTCTTAGGCGAAACCCGACGAGAAACAAAGCTGTGATATATGC	960
QY	961	AAGGCGUAGUUGGACUAGAGAUCCACUACUUCUUAGUUUGCGGGUUCACUUAUAG	1020
Db	961	AAGGCGCAATGGAGACTGAGAAATCAAGCTCATCTTCAAGCTTGTGGGTTCACATTTAA	1020
QY	1021	AGAACAGCGCGAUUCACUAGCAAGAGAGAGAAAGAGUCUUACGGGCAUUCUUCAACA	1080
Db	1021	AGAACAGCGGGGTCTCTCATTCAAAGAGAGAGAAAGATGCTTACAGGCAATCTCCAAACA	1080
QY	1081	UUGAAAAUAAGGUGUGCAUAGGAGUAACGAGAGAUUCACAUUGUGGAAAAAGGCAACA	1140
Db	1081	TTGAAAAATTAAGATGTCATGAGGGGTACGAGAGATTCAAAATGCTGGGGAAGGGCAACA	1140
QY	1141	GUUAUAUCUAGAAAAAGCAACAGAGAGAUUGAUUCAGUCUUAUUGUGAGAGAGACGAA	1200
Db	1141	GCTAATACCTGAAAAAGCAACAGAGAAATTTGTTCAAGCTCATGTGAGTGGAAAGGACAA	1200
QY	1201	CAGUCGUAUAGCUGAAGCAUAUAUUGUGGCGCAUUGUUCACAGAAAGAUUUGUAUUA	1260
Db	1201	CAGTCAATATGCCGAAACAAATATCTGATGCCATGTGGTTCACAAAGAGATTGCATGTATA	1260
QY	1261	AAAGCAGUUAAGUGUGUUCUGAUUUCGUUAUAAGGGCAAAUACAGCGAUUGAUUCCCAAG	1320
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QY	1381	GAACCAUUAUCGACAUAUGUUGGGAUUGAUUGGGGUUAUUAACGACAUUGCAUUCAMAGACA	1440
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[illegible]

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 XX MO9639179-A1.  
 XX 12-DEC-1996.  
 XX 03-JUN-1996; 96WO-US08441.  
 XX 05-JUN-1995; 95US-0462388.  
 XX (AVIR-) AVIRON.  
 XX Coelighn KT, Parkin NT;  
 XX WPI: 1997-042859/04.  
 XX P-PSDB: AAM07706.  
 XX  
 PT Recombinant influenza virus with mutation(s) in charged cluster  
 PT regions - esp. temperature-sensitive mutation(s), has attenuated  
 PT phenotype suitable in vaccines for preventing influenza  
 ' .  
 Ps Claim 7; Page -; 39pp; English.  
 XX The sequences given in T75683-90 encode modified influenza virus PB2  
 CC proteins, ALA1-ALA8. The modified proteins are generated by replacing  
 CC certain Arg, Lys and Asp residues in one of 8 charged clusters  
 CC identified in influenza A virus A/LA/2/87 PB2 protein, with Ala  
 CC residues. Specifically, the mutations are as follows: ALA1 (residues  
 CC 2-6) ERIKE -> EAIAR, ALA2 (residues 120-124) DKVER -> DAVEA, ALA3  
 CC (residues 140-144) KIRRR -> KIRAA, ALA4 (residues 187-192) KEKKEE ->  
 CC KEAAEE, ALA5 (residues 339-343) KREER -> AAEEB, ALA6 (residues 677-681)  
 CC EDPDE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8  
 CC (residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which  
 CC contain these mutations produce attenuated viral phenotypes, useful as  
 CC master donor viruses in the preparation of immunogenic compositions,  
 CC e.g. vaccines, for preventing influenza, or a disease associated with  
 CC influenza infection. Modification of charged cluster residues results  
 CC in consistent and predictable exhibition of temperature sensitivity.  
 CC These sequences are not given in the specification and are based on the  
 CC influenza virus A/Memphis/8/88 given in Genbank M73517.  
 XX  
 XX Sequence 2341 BP; 802 A; 426 C; 575 G; 538 T; 0 other;  
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 Query Match 89.2%; Score 2088.2; DB 18; Length 2341;  
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KW Influenza A virus A/La/2/87; ALA1; ALA2; ALA3; ALA4; ALA5; ALA6;
KW ALA7; ALA8; attenuation; viral phenotype; temperature sensitivity;
KW vaccine; influenza virus A/Memphis/8/88; ss.
OS Influenza virus.
XX Synthetic.
FH Key
FT CDS Location/Qualifiers
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FT /*tag= a
FT /product= ALA3
EN MO9639179-A1.
XX 12-DEC-1996.
PD 03-JUN-1996; 96MO-US08441.
XX 05-JUN-1995; 95US-0462388.
XX (AVIR-) AVIRON.
PA Coeligh KL, Parkin NT;
PI WPI: 1997-042859/04.
XX P-PSDB; AAM07707.
DR Recombinant influenza virus with mutation(s) in charged cluster
XX regions - esp. temperature-sensitive mutation(s), has attenuated
XX phenotype suitable in vaccines for preventing influenza
XX Claim 7; Page -: 39pp; English.
XX
XX The sequences given in T75683-90 encode modified influenza virus PB2
XX proteins, ALA1-ALA8. The modified proteins are generated by replacing
XX certain Arg, Lys and Asp residues in one of 8 charged clusters
XX identified in influenza A virus A/La/2/87 PB2 protein, with Ala
XX residues. Specifically, the mutations are as follows: ALA1 (residues
XX 2-6) ERIKE -> EAIAE, ALA2 (residues 120-124) DKVER -> DAVEA, ALA3
XX (residues 140-144) KIRRR -> KIIAA, ALA4 (residues 187-192) KEKKEE ->
XX KEAAEE, ALA5 (residues 339-343) KRREE -> AAREE, ALA6 (residues 677-681)
XX EDDEE -> EAPPA, ALA7 (residues 699-703) KEDRR -> KEDAA and ALA8
XX (residues 736-740) KRKRD -> ARKRD. Recombinant influenza viruses which
XX contain these mutations produce attenuated viral phenotypes, useful as
XX master donor viruses in the preparation of immunogenic compositions,
XX e.g. vaccines, for preventing influenza, or a disease associated with
XX influenza infection. Modification of charged cluster residues results
XX in consistent and predictable exhibition of temperature sensitivity.
XX These sequences are not given in the specification and are based on the
XX influenza virus A/Memphis/8/88 given in Genbank M73517.
SO Sequence 2341 BP; 803 A; 426 C; 575 G; 537 T; 0 other;
QY Query Match 89.2%; Score 2088.2; DB 18; Length 2341;
DB Best Local Similarity 71.5%; Pred. No. 0;
DB Matches 1674; Conservative 509; Mismatches 158; Indels 0; Gaps 0;
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Db	1441	GAGATGTCAATGAGAGGAATTAAGATGACACAAATGGGGGTGGATTAAATATCTCCAGACACA	1500
Oy	1501	GAGAGUAUAGUGUGAGCAUUGACCGGUTUUUGAGAUUGAGACCAACGAGGAUAUUGUA	1560
Db	1501	GAGAGGGTGTGGTGTAGCATTTGATCGATTTTGTGAGAGTTTGAGACCAGTGGGAATTGTA	1560
Oy	1561	CUACUAUCUCUCUAGAGAGUGCAUGGAAACAAGGAAACAGAGAAACUGACAUAUACUUAAC	1620
Db	1561	TTACTATCTCTCTGAGAGAGGTCACTGAAACAACAGGAAACAGAGAGACTGACAAATPACTTAC	1620
Oy	1621	UUAUCUGUAUAGUAGUGGGAGAUUAUUGGCCUGAGUCAGUGUGUGUUAUACUUAUCUUAAG	1680
Db	1621	TCATCGTCAATGATGTGGGAGATTTAAACGGCCCTGAGTGGTGTGGTCAATPACTTATCA	1680
Oy	1681	UGAUUCUAUCAGAAACUGGGAAACUGUUAUAUUCAGUGUGUCUACAGUCCUAACUAGUCUA	1740
Db	1681	TGGATTCATCAAGAAATTGGGAAACGTTTAAATTCATATGATCTCAGAAATCTCGAAATGTTG	1740
Oy	1741	UACAAUAAAAUUGAAUUUUUGAGCCAUUUCACUUCUUAUGUCUUAAGCCAUUUAAGGCCAA	1800
Db	1741	TACAAACAAATTGGAAATTTGAACCATTTCACTTTAGTTCTTAAGGCCATTTAAGAGGCCAA	1800
Oy	1801	UACAGUGGUUUUGUUAAGACUCUUAUUCCAAACAUAUGAGGGAUUAUCUUGGGAGACUUAUUGAU	1860
Db	1801	TACAGTGAATTTGTCAACAACCTTAATTTCCAACAATGAGAGATGTACTTGGGACATTTGAT	1860
Oy	1861	ACCAACCCAGATPAAPAAACUUUCUUCUUGSCUUGSCAGCCGCCCAACCAAGCAAAUGAGUAUG	1920
Db	1861	ACCAACCCAGATPAAPAAAGCTTCTCTCTTTTGACGCCCTCAACCAAAAGCAAAAGAGAGATG	1920
Oy	1921	CAGUUCUCUUCACUGACUCUGUAUUGUGAGGGGAGUCAGAGAAUUGAGAAUUAUCUUGAAGGGC	1980
Db	1921	CAGTTCCTCTCATTTGACGTGTGAATGTGAGGGGATCAGGGATGAGAAATATCTTTGTAAAGGGC	1980
Oy	1981	AAUUCUCCUUAUUAUUCACUAACAAACCAACUAAGACUUAACAUAUUCUCGAGAAAGAU	2040
Db	1981	AATTCCTCTGTATTCACCTACAAACAAACCACTTAAAGACTTAAACAAATTTCTGGAAAAAGAT	2040
Oy	2041	GTUGGCAAUUUAACUGAAGACCCAGAGUAGAGGCAACUUGGGAGUGGAGUCCGCTGUCUUG	2100
Db	2041	GCTGGACATTTAAATTTGAAGACCCAGATGAAAGCACHTCGGAGTGGAGTCCGCTGTCTTG	2100
Oy	2101	AGAGAGAUUCUCUAUUCUGGGCCAAAGAGAUAGUAUUGACCAAGCAUUAAGCAUACAU	2160
Db	2101	AGAGGATTTTCATTTCTAGTGAAGAGAGACAGAGATACGGACCAAGCATTTAAAGCATCAAT	2160
Oy	2161	GAAUCGAGUAAACUUGGCCAAAGAGAAAGCCUAUUGUAUAUAUUGGGCAAGGAGAGCGUG	2220
Db	2161	GAACTGAGTAACTTTGCAAAAGGGGAAAAAGGCTAATGTGCTPAAATTTGGGCAAGAGACGTG	2220
Oy	2221	GGUUGUGUAUUGAAACGAAAAACGAAACUUCUUGACUAUCUAACUGACAGCCAGACAGCAC	2280
Db	2221	GGTGTGGTAATGAACGAAAAACGGGACCTTGACATCTTACTGACAGCAACAGCGGACC	2280
Oy	2281	AAAAGAUUCGGAGUGGCCAUCAUAUUAUGUUGAAUAGUUAUAAAAACACUUGUUCUAC	2340
Db	2281	AAAAGAAATTCGGATGGCCATCAATTAATGTGAATAGTTAAAAACGACCTTGTCTTAC	2340
Oy	2341	U 2341	
Db	2341	T 2341	

## RESULT 12



[illegible]

QY	2341 U 2341	
DB	2341 T 2341	
	RESULT 13	
	AAD15675	
	ID AAD15675 standard; DNA; 2341 BP.	
XX		
AC	AAD15675;	
XX		
DT	15-NOV-2001 (first entry)	
XX		
DE	Equine influenza virus H3N8 neicaiPB22341 DNA.	
XX		
KM	Equine influenza virus; ei: cold adaptation; temperature sensitivity;	
XX	vaccine; neicaiPB22341 DNA; PeicaiPB2759 protein; ds.	
OS		
XX	Equine influenza virus H3N8.	
FT		
FT	Key	Location/Qualifiers
FT	CDS	28..2307
FT		/tag= a
FT		/product= "PeicaiPB2759 protein"
FT	misc_feature	28..2304
FT		/tag= b
FT		/note= "This region is specifically claimed as
FT		SEQ ID NO: 29 in claim 2 of the specification"
XX		
PN	WO200160849-A2.	
XX		
PD	23-AUG-2001.	
XX		
PF	16-FEB-2001; 2001WO-US05048.	
XX		
PR	16-FEB-2000; 2000US-0506286.	
XX		
PA	(UYP1-) UNIV PITTSBURGH.	
XX		
PI	Dowling PW; Youngner JS;	
XX		
DR	WP1; 2001-522584/57.	
XX	P-PSDB; AAE09026.	
XX		
PT	Novel isolated equine influenza virus (wild-type and cold-adapted)	
PT	proteins and viruses containing nucleic acid molecules encoding the	
PT	proteins, which are useful for protecting animals from influenza virus	
PT	infections -	
XX		
PS	Claim 2; Page 64-67; 172pp; English.	
XX		
CC	The patent discloses cold-adapted equine influenza viruses and	
CC	reassortant influenza A viruses comprising atleast one genome	
CC	segment of such an equine influenza virus, wherein the equine	
CC	influenza virus genome segment confers atleast one identifying	
CC	phenotype of the cold-adapted equine influenza virus, such as	
CC	cold adaptation, temperature sensitivity, dominant interference	
CC	or attenuation. The viruses are useful for protecting animals	
CC	from diseases caused by influenza viruses. They are also used	
CC	as vaccines. The present sequence is equine influenza (ei) virus	
CC	H3N8 neical (cold adapted) PB22341 DNA encoding PeicaiPB2759	
CC	protein.	
XX		
XX		
SO	Sequence 2341 BP; 812 A; 443 C; 564 G; 522 T; 0 other;	
QY	Query Match	77.0%; Score 1801.8; DB 22; Length 2341;
	Best Local Similarity	66.1%; Pred. No. 0;
	Matches 1547; Conservative 457; Mismatches 337; Indels 0; Gaps 0	
1	AGCGAAAGCAGGUCAUUUUUCAGUUGGAGAAAGAAAGAAACGACUACGACUAGCAGG	60
1	AGCAAAAGCAGGTCGAAATATTTTCATATTTGAGAGCAATATMAAGAACTGAGACATCTAATG	60

[illegible][illegible]

**D**b 2221 GTGTTGGTAATGAAGAACGSAAAGCGTCACTCTTGACAATTACTGTGACAGCCAGACAGCGACC 2280  
**Q**y 2281 AAAAAGAUUUCGGAUGGCCAUCAUUAUUGUUGAUAUUGUUAAAAACGACCUUGUUUCUAC 2340  
|||||||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||  
**D**b 2281 AAAAGAAATTCGATGCGCATCAATTAGTGTTGAATGTTTTAAAACGACCTTGTTCTAC 2340  
**Q**y 2341 U 2341  
+  
**D**b 2341 T 2341

**R**ESULT\_14  
**I**D AAZ50977 standard; DNA; 1241 BP.  
**A**C AAZ50977;  
**X**X  
**D**T 05-JUN-2000 (first entry)  
**F**r Wild type equine influenza virus H3N8 PB2-N protein DNA.

**K**. RNA-directed RNA polymerase; wild type PB2-N protein; horse;  
**K**m cold-adaptation; reassortant virus; temperature sensitivity; attenuation;  
**K**w antiviral; vaccine; prevention; treatment; dominant interference;  
**M**k Influenza A virus infection; ds.  
**X**X  
**O**S Equine influenza virus H3N8.  
**X**X  
**X**H Key Location/Qualifiers  
**F**H 28..1239  
**T**T /\*tag= a  
**F**T /product= "PB2-N protein"  
**F**T /note= "Encodes N-terminal portion of PB2 protein"  
**F**T /partial  
**F**T misc\_feature  
28..1241  
/\*tag= b  
**F**T /note= "This region is specifically claimed"

**X**X WO200009702-A1.  
**P**N 24-FEB-2000.  
**X**X 12-AUG-1999; 99WO-US18583.  
**P**F 13-AUG-1998; 98US-0133921.  
**X**X (UPI-) UNIV PITTSBURGH.  
**P**A Dowling PW, Youngner JS;  
MPI; 2000-224339/19.  
**D**R P-PSDB; AAV70058.  
**X**X New cold-adapted equine influenza viruses and reassortant viruses used  
**P**T as vaccines for treating influenza infections in animals, particularly  
**P**T horses, have a phenotype such as temperature sensitivity or dominant  
**P**T interference -  
**X**X  
**P**S Claim 8; Page 96-99; 127pp; English.

The patent discloses experimentally generated cold-adapted equine influenza viruses, and reassortant influenza A viruses comprising at least one genome segment of the cold-adapted virus, which confers at least one identifying phenotype selected from cold-adaptation, temperature sensitivity, dominant interference and attenuation. These viruses are used in therapeutic compositions e.g. vaccines for preventing or treating infections caused by influenza A viruses in animals, particularly horses. The present sequence is a DNA (nucleotide) encoding N-terminal portion of wild type PB2 protein (PcPB2-NM04), an RNA-directed RNA polymerase, from equine influenza virus HN8. This sequence is modified to generate cold-adapted equine influenza virus.

[illegible]



QY 1021 AGAACAAGCGGATCAUCAGUCGACAGAGAGAGAAAGUGCTUACGGGCAUUCUCAAACA 1080  
 |||||  
 DB 1021 AGAACAAGCGGATCAUCAGUCGACAGAGAGAGAAAGUGCTUACGGGCAUUCUCAAACA 1080  
 |||||  
 QY 1081 UUGAAAUAAAGGUGCAGAGGAGUACGAGAGUUCACAUUGUGGAGAAAGGCGAACA 1140  
 |||||  
 DB 1081 TTGAAATTAAGATGCTAGAGGCTATGAAAGATTCAATGATGCGAAGAGAGCAACA 1140  
 |||||  
 QY 1141 GCUAUAUCUAGAAAGCAACGAGAGAUUGUACACUGAUNUGUGAGAGAGAGAGAA 1200  
 |||||  
 DB 1141 GCCATTCTCAGAAAGCAACGAGAGATTGATTCATATGATAGTAGTGAGAGATGAA 1200  
 |||||  
 QY 1201 CAGUCGAGUGCUGACGAAUAAUUGUGGCGCAUUGUUC 1241  
 |||||  
 DB 1201 CAATCAATGCTGAGCAATTAATGATGATGCTGTTTC 1241  
 |||||  
 RESULT 15  
 15664  
 AAD15664 standard; DNA; 1241 BP.  
 AAD15664;  
 15-NOV-2001 (first entry)  
 Equine influenza virus H3N8 neiwCPB2-N1241 DNA.  
 Equine influenza virus; ei; cold adaptation; temperature sensitivity;  
 vaccine; neiwCPB2-N1241 DNA; PeiwCPB2-N404 protein; de.  
 OS Equine influenza virus H3N8.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 28..1239  
 FT /tag= a  
 FT /product= "PeiwCPB2-N404 protein"  
 FT /note "CDS does not include stop codon"  
 FT /partial  
 FT 28..1241  
 FT misc\_feature  
 FT /tag= b  
 FT /note "This region is specifically claimed as  
 FT SEQ ID NO: 7 in claim 2 of the specification"  
 FT  
 FN WO200160849-A2.  
 XX  
 PD 23-AUG-2001.  
 PR 16-FEB-2001; 2001WO-US05048.  
 XX  
 XX 16-FEB-2000; 2000US-0506286.  
 XX (UPI-) UNIV PITTSBURGH.  
 XX  
 XX Dowling PM, Youngner JS;  
 DR WPI; 2001-522584/57.  
 DR P-PSDB; AAE09021.  
 XX  
 PT Novel isolated equine influenza virus (wild-type and cold-adapted)  
 PT proteins and viruses containing nucleic acid molecules encoding the  
 PT proteins, which are useful for protecting animals from influenza virus  
 PT infections  
 XX  
 XX Claim 2; Page 41-43; 172pp; English.  
 XX  
 CC The patent discloses cold-adapted equine influenza viruses and  
 CC reasortant influenza A viruses comprising at least one genome  
 CC segment of such an equine influenza virus, wherein the equine  
 CC influenza virus genome segment confers at least one identifying  
 CC phenotype of the cold-adapted equine influenza virus, such as  
 CC cold adaptation, temperature sensitivity, dominant interference  
 CC or attenuation. The viruses are useful for protecting animals

CC from diseases caused by influenza viruses. They are also used  
 CC as vaccines. The present sequence is equine influenza (ei)  
 CC virus H3N8 neiw (wild type) PB2-N1241 DNA encoding PeiwCPB2-N404  
 CC protein.  
 XX  
 SQ Sequence 1241 BP; 462 A; 231 C; 292 G; 256 T; 0 other;  
 Query Match 41.2%; Score 964.2; DB 22; Length 1241;  
 Best Local Similarity 68.0%; Pred. No. 2.86-269;  
 Matches 844; Conservative 224; Mismatches 173; Indels 0; Gaps 0;  
 QY 1 AGCGAAGCAGAGAUUUAUUAUUGAAGAAUUAAGAAUUAAGCAUUCGAAUUG 60  
 1 AGCAAAAGCAGAGTAATAATATATGCAATATGAGAGATTAAGAAATGAGATCTAATG 60  
 DB 1 AGCAAAAGCAGAGTAATAATATATGCAATATGAGAGATTAAGAAATGAGATCTAATG 60  
 QY UCGAGUCUCCACUCCGAGAUUACUAAACCAACAGUGAGCCAUUAGGCCAUU 120  
 61 TCACATTCGCCACCCGAGATCTAACAACCACTGTCGACCACTGACATATATC 120  
 DB 61 TCACATTCGCCACCCGAGATCTAACAACCACTGTCGACCACTGACATATATC 120  
 QY 121 AAGAAUACACUACGAGGAGCAGAAAGAAACCCGUCACUUGAGUAGAAUUG 180  
 121 AAGAAUACACUACGAGGAGCAGAAAGAAACCCGUCACUUGAGUAGAAUUG 180  
 DB 121 AAGAAUACACUACGAGGAGCAGAAAGAAACCCGUCACUUGAGUAGAAUUG 180  
 QY 181 GCAUAGAAUUVCCGATUACGCCGACAGAGUUAACAGAAUAGUUCUGAGAAU 240  
 181 GCAATGAAATCCCAATTTACGAGATAGAGATTAATGAAATGATTCCTGAGAGAAAT 240  
 DB 181 GCAATGAAATCCCAATTTACGAGATAGAGATTAATGAAATGATTCCTGAGAGAAAT 240  
 QY 241 GAGCAAGGCGAAACUUAUUGAGUAAUUGUGUACCGGAGUUGCGUUGAGU 300  
 241 GACAGGGGCAAAACCTTTGAGCAAAACGACATCTGCTGACGCGGTATAGSTA 300  
 DB 241 GACAGGGGCAAAACCTTTGAGCAAAACGACATCTGCTGACGCGGTATAGSTA 300  
 QY 301 UCACCTUCGUGAGUAGUUGAGUAAUUGAACCAUUGACAGUAGGUGUUAU 360  
 301 TCACCTTCGAGAGATGATGTAATGAGATGAGACCAACAGACCAATTCATTAT 360  
 DB 301 TCACCTTCGAGAGATGATGTAATGAGATGAGACCAACAGACCAATTCATTAT 360  
 QY 361 CCAAAAUCUACAAACUUAUUGAGAAAGUCAAAGGUAUUAACUUGGACCU 420  
 361 CCAAAAGCTTACAAACCTTTATTTGAAAAGTTGAAAAGATTAAACCGAAACCTTTGGC 420  
 DB 361 CCAAAAGCTTACAAACCTTTATTTGAAAAGTTGAAAAGATTAAACCGAAACCTTTGGC 420  
 QY 421 CCUGUCCAUUUUAGAAACCAAGUCAAUUAUUGCGGAGAGUGACAUAAUUCUGU 480  
 421 CCCGTTATTTAGAAATCAAGTAAAGTAAAGAGAGTTGATGTAACCCGCTGC 480  
 DB 421 CCCGTTATTTAGAAATCAAGTAAAGTAAAGAGAGTTGATGTAACCCGCTGC 480  
 QY 481 GCAGACCUCAUGUGCAAGAGAGCACAGAGUUAUUGAGAGUUGUUCUUAACGA 540  
 481 GCGACCTCAGTGCCAAAGAAAGCAGAGATGTATCAATGAAATGTTTCCCAAATGA 540  
 DB 481 GCGACCTCAGTGCCAAAGAAAGCAGAGATGTATCAATGAAATGTTTCCCAAATGA 540  
 QY 541 GUGGGGCGCAGAGAUUACUAGUGGAAUUGCCAAUUAUUAUUAACCAAGAGAA 600  
 541 GTGGAGGCCAGAAATTTCTAATCGAATCAACAATTAACAATTAACAAGAGAAAGAA 600  
 DB 541 GTGGAGGCCAGAAATTTCTAATCGAATCAACAATTAACAATTAACAAGAGAAAGAA 600  
 QY 601 GAACUCCAGAUUUGCAAAAUUUAUACCUUUGAGUUGCGUUAUUGUAGAGAA 660  
 601 GAACUCCAGAUUUGCAAAAUUUAUACCUUUGAGUUGCGUUAUUGUAGAGAA 660  
 DB 601 GAACUCCAGAUUUGCAAAAUUUAUACCUUUGAGUUGCGUUAUUGUAGAGAA 660  
 QY 661 GUCCGAAAAAGAGAUUUCUCCAGUUGCUGUGAGAAACAGAGUGUUAUUGAG 720  
 661 GTCCGAAAAACAGATTCTCCAGTGGCTGGCGGAACAGAGATGATCATTTGAAGTG 720  
 DB 661 GTCCGAAAAACAGATTCTCCAGTGGCTGGCGGAACAGAGATGATCATTTGAAGTG 720  
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 DB 721 TTGCATCTGACTCAGGAGACATGCTGGGACAAATGATACCCAGAGAGAGAGATTAGA 780  
 QY 781 AUAUGAUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 781 AUAUGAUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 DB 781 AUAUGAUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840  
 QY 841 GUUUCAGAGAUUCACUAGUUAUUGAGAUUGAGUAGUAGUAGUAGUAGUAG 900  
 841 GTATCAGACATTCACATGAGATCCCTGCTGGAATGTGCGACAGTACACAGATTGGTGA 900  
 DB 841 GTATCAGACATTCACATGAGATCCCTGCTGGAATGTGCGACAGTACACAGATTGGTGA 900  
 QY 901 ACAAGAGUGUGACAUUUCUUGAGCAAGAACCAACAGAGAGAGAGAGAGAG 960  
 901 |||||

```
Db      901 ATAAGAGTGTAGACATCTCTTAAGCAAAATCCAAACAGAGAAACAAGCTGTGATATATGC 960
Qy      961 AAGGCTGCAUUGGGAUCUGAGAUUCAGCTUCCUUCAGUUUUGGCGGCUUCAUUUAAG 1020
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      961 AAGGCGCAATGGGGTTAAGAAATTAGCTCATTCAGCTTTGGTGGATTGACCTTTAAG 1020
Qy      1021 AGAAACAAGCGGUAUCAGUCAAAGAGAGAAAGAAAGUGCUUACGGGCAUUCUCAAACA 1080
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1021 AGAAACAAGTGGATCATCAGTCAAGAGAGAAAGAAATGCTTACGGGCAACCTTCAAACA 1080
Qy      1081 UUGCAAAAUAAAGGUGCAUGAGGGAUUCGAGAGUUCACAUGUUGGGAAAGGGCAACA 1140
      ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1081 TTGAAAAATAGAGGTGATGAGAGGCTATGAGAAATTCACATGAGTGGAGAAAGAGCAACA 1140
Qy      1141 GCUAUAUCUGAAAGCAACACAGAGAUUGAUUUCAGCTUAGUUGUGAGUGAAAGACGAA 1200
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1141 GCCATTCTCGAAGAGGCAACACAGAAAGATTGATTCATTGATAGTAGTAGTGAGAGATGAA 1200
Qy      1201 CAGUCGUAUGCUGAAGCAAUUAUUGGCGCAUGGUUAUUUC 1241
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1201 CAATCAATTGCTGAGCAAAATTAATTGTAGCCATGTGTGTTTC 1241
```

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Job time : 611 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 16:26:30 ; Search time 163 Seconds

**Title:** US-08-573-569-15

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Post-processing: Minimum Match 0%

Database : Issued\_Patents\_NA: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1806.6	77.2	2341	4	US-09-506-286B-44	Sequence 44, App
2	1801.8	77.0	2341	4	US-09-506-286B-47	Sequence 47, App
3	1749	74.7	2277	4	US-09-506-286B-46	Sequence 46, App
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4	1744.2	74.5	2277	4	US-09-506-286B-49	Sequence 49, App
5	964.2	41.2	1241	4	US-09-506-286B-13	Sequence 13, App
6	964.2	41.2	1241	4	US-09-762-861B-13	Sequence 13, App
7	962.6	41.1	1241	4	US-09-506-286B-16	Sequence 16, App
8	962.6	41.1	1241	4	US-09-762-861B-16	Sequence 16, App
9	941.4	40.2	1232	4	US-09-506-286B-22	Sequence 22, App
10	941.4	40.2	1232	4	US-09-762-861B-22	Sequence 22, App
11	941.4	40.2	1233	4	US-09-506-286B-19	Sequence 19, App
12	941.4	40.2	1233	4	US-09-762-861B-19	Sequence 19, App
13	940.4	40.2	1214	4	US-09-506-286B-15	Sequence 15, App
14	940.4	40.2	1214	4	US-09-762-861B-15	Sequence 15, App
15	938.8	40.1	1214	4	US-09-506-286B-18	Sequence 18, App
16	938.8	40.1	1214	4	US-09-762-861B-18	Sequence 18, App
17	938.2	40.1	1232	4	US-09-506-286B-23	Sequence 23, App
18	938.2	40.1	1232	4	US-09-762-861B-23	Sequence 23, App
19	907.6	38.8	1194	4	US-09-506-286B-21	Sequence 21, App
20	907.6	38.8	1194	4	US-09-762-861B-21	Sequence 21, App
21	904.4	38.6	1194	4	US-09-506-286B-25	Sequence 25, App
22	904.4	38.6	1194	4	US-09-762-861B-25	Sequence 25, App
23	66.4	2.8	7218	1	US-08-213-463-14	Sequence 14, App
24	49.2	2.1	62	1	US-08-462-388-7	Sequence 7, App
25	44.6	1.9	60	3	US-09-614-971-12	Sequence 12, App
26	44.6	1.9	60	4	US-10-001-845-12	Sequence 12, App
27	44.6	1.9	60	4	US-10-001-845-12	Sequence 12, App

28	43.2	1.8	777	4	US-09-328-355-499	Sequence 499, Appl
29	37.2	1.6	2377	1	US-08-676-967-2	Sequence 2, Appl
30	37.2	1.6	2377	1	US-08-676-978-2	Sequence 2, Appl
31	37.2	1.6	2277	2	US-09-098-487-2	Sequence 2, Appl
32	36.6	1.6	43	3	US-08-604-757-7	Sequence 7, Appl
33	36.6	1.6	43	3	US-09-612-951-7	Sequence 7, Appl
34	36.6	1.6	43	4	US-10-001-845-7	Sequence 7, Appl
35	36.6	1.6	705	4	US-09-107-533A-2869	Sequence 2869, Appl
36	36.2	1.5	168375	4	US-09-426-290-1	Sequence 1, Appl
37	35.2	1.5	315	4	US-09-107-533A-1416	Sequence 1416, Appl
38	35.2	1.5	762	4	US-09-107-533A-1418	Sequence 1418, Appl
39	35.2	1.5	816	4	US-09-107-533A-1417	Sequence 1417, Appl
40	35.2	1.5	1664976	4	US-08-996-421B-1	Sequence 1, Appl
41	34.8	1.5	617	4	US-09-321-017B-446	Sequence 446, Appl
42	34.4	1.5	865	3	US-09-328-111-128	Sequence 128, Appl
43	34.2	1.5	204	4	US-09-696-556-6	Sequence 6, Appl
44	34	1.5	319608	4	US-09-539-33D-1	Sequence 1, Appl
45	34	1.5	319608	4	US-09-679-409-1	Sequence 1, Appl

## ALIGNMENTS

## RESULT 1

; Sequence 44, Application US/09506286E

GENERAL INFORMATION

APPLICANT: Youngner, Julius S.

TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

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CONSTRUCTION. EQUINE INFLUENZA VIRUS MONO  
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QY	301	UCACCCUCUCUGUCGUAUGUGGAAUUGAAAUUGGACCAUUGACCAAGAACCGUUCUAU	360
Db	301	TCACCTTGCGACGTGACATGTGTGGAAATAGAAATGACCAACAACGACCAATTCATAT	360
QY	361	CCAAAUAUUCACAAAUCUUAUUUUGAGAAAGUCGAAAGGUTUAAAUAUGGAACTUUGGC	420
Db	361	CCAAAAGCTACAAAACCTTATTTTGAAAAAGTTTAAACACGSAACCTTTGGC	420
QY	421	CCUGUCACUUUUGAGAAACCAAGUCAAAUAAGCCCGAAGGTGACUAUAUUCUGUCU	480
Db	421	CCGTTCACTTAAAGGATCAAGTCAAGATPAACGAGGTTGAATGTAAACCTGTGC	480
QY	481	GCAGACUCUACGUGCCAGAGGCGACAGAGUUGUAUUCAGUAGUUGUUTUCCUAAACGA	540
Db	481	GCGACCTCAAGTCCAGAAAGACACAAAGATGATCATGGAAGTTTGTTCCTCCAAATGA	540
QY	541	GUGGGGGCCAGGAUACUAAGUCGCGAATUCGCAUUAUACUAUACCAAGAGAAAAAGA	600
Db	541	GUGGAGGCCAGAAATTTCTAAATCTCGAATCAACAATPAATCAAAAGAGAAAAAGAA	600
QY	601	GAACTCCAGAGATUGGCAAAAUUUCACUUUUGAGUGGUGGCUACUUVUAGAGAAACU	660
Db	601	GAACTTCAGACTCGCAAAATTCCTCCCAAGTGTGCGGAAACAAAGATGTAACTTAAGT	660
QY	661	GUCCGAAAAACGAGAUUUDUCCCAAGUGUCUGUGUGAGCAAGCAGUGUUGACUUGA	720
Db	661	GTCGAAAAAACAAAGATTCCTCCCAAGTGTGCGGAAACAAAGATGTAACTTAAGT	720
QY	721	UUGCACUUGACUCCAAAGAAACAGUCUGGAAACAGAGUACUUCACAGUGGAGAAAG	780
Db	721	TTGCACTCGAATCTCAGAGAAACATGCTGGGAAACAAATGTAAACCCAGAGAGAAATTTGA	780
QY	781	AAUGAUGAUGUGUGAUCAAAGUCUAAUUAUUGAGAGCCAGAGAGAUUGAGAAAGACACA	840
Db	781	AACGATGACATTGATCTAAAGTTTAATTAATTCGTCCCGGAAACATGTAGAAAGACGACA	840
QY	841	GUUACAGACAGAUCCACUAGCUCUUUAUUGAGAUUGCCACACAGACACACAUUGCCGG	900
Db	841	GTATAGACAGATCCACTAGCATCCCTGCTGGAAGTGTCCAAAGTACACAGATTGTGTGA	900
QY	901	ACAAAGAUUGUGACAUUUCUUUUGAGCAACCCAAACGAAAGACAAAGCUGUGGAAUUAUG	960
Db	901	ATPAGAGATGTAGACATCTCTTAAGCAGAAATCCAAACAGAGAAACAAAGCTGTGATATATGC	960
QY	961	AAAGCUGCAUUGGAGCUGAGAGACUCUCUUCAGUUVUUGCCGGUUCACAUUUAAG	1020
Db	961	AAAGCAGCAATGGGGTTTAAGATTAGTCATCATTTCAAGCTTTGTGTGATTCACTTTAAG	1020
QY	1021	AGAACCAAGCGGUAUUCAGUCUCAAAGAGAGAAAGAGUUCUUGCGGCAUUCUUAACA	1080
Db	1021	AGAACCAAGGTGATCATCTCACTCAAGAGAGAAAGAAATGCTTACGGGCAACCTTTAAACA	1080
QY	1081	UUGAAAAUAAGGUGUCUUGAGGGAUAACGAGAGUUCACAAUGGUGUGGAAAAAGGCAACA	1140
Db	1081	TTGAAAAATPAGAGTGCATGAAGCGTATGAAAGATTCAACATGTGTGGAAGAAAGACAAACA	1140
QY	1141	GCUAUACUCAGAAAAAGCAACGAGAGAUUGAUUCAGUCUUAUGAGUGGAAAGACAGAA	1200
Db	1141	GCCATTTCTCAGAAAGCAACGAAAGATTGATTTCAATTGATGTAAAGTGGGAGAGATGATA	1200
QY	1201	CAGUCGUAUGCUGAAGCAUAUUAUUGGCGCAUGUAUUUUCAAAGAAAGAUUGUUGUA	1260
Db	1201	CATCAATATTCCTGAAGCAATTAATGTAGCCATGTGTGTTTTCGAAAGAAATTTGCATGATA	1260
QY	1261	AAAGCAGUUAAGGUGUCUGAGAUUDUCGUUAUUAAGGCAAAUCACGAGUUAUUCCAUG	1320
Db	1261	AAAGCAGTTTCAAGGCGCATTTGAACCTTCGTTAATAGAGCAAAATCAGGCTTTGAACCCCATG	1320
QY	1321	CAUCAAACUUUUAAGCAUUAUUUGAGAAAGUUGGAAAGUCUUUUUCAAUAUUGCGGAAU	1380
Db	1321	CATCAACTCTTGAAGGATTTCCAAAAAGATGCAAAAGTCTCTTTCCAGAAATGTGGGAGAT	1380

QY	1381	GAACAUUUCGAAUUGUGAUGGAGAUUUAUUGGGGUAUUAACAGACAGUAUUCACAAAGACA	1440
Db	1381	GAACCCATTCGACATGTGATGGGAATATTTGGATTTTGGCTGACATGACCCCAAGCAC	1440
QY	1441	GAGAGUGCAUAGAGAGGGGUAAGUGACGCAAAAUGGGCCUAGUGAUAUUCUCCAGCGCG	1500
Db	1441	GAGATGTCAATTGAGAGGAGTGAAGCAGCAAAAATGGGAAGTGAATGATCTCCAGACT	1500
QY	1501	GAGAGAUUAUGUGAGACAUUAGCCGGUUUUUGAUAUUGAGCCAAACGAGGAUAUGUA	1560
Db	1501	GAGGAGATGTGGTGAGCATTGACCGTTTTTAAAGATTTGGGATTCAAAGGGGAAACATA	1560
QY	1561	CUACUUAUCUCCUGGAGAGGUCAGUGAAGAACACAGGGAAACAGAGAAUCUGACAUUAUCUAC	1620
Db	1561	CTACTGTCTCCCTGAAGAGGTCTAGTAAACACAGAGAAACGAGAAAGCTGACATTAATTTAT	1620
QY	1621	UGAUCGUAUAGUUGGGGAGAUUAUGGCCUGAGUGUCAGUGUGUGUAUUAUCUACUACG	1680
Db	1621	TCATCATCAATAGATGGGAGATTAATATGATCCGAATCAGTGTGGTCAATATCAATCA	1680
QY	1681	UGAUCUUAUCGAAACUUGGAAACUGUUAUAUUGAGUGUCUGAUAUUCUACUACUACUA	1740
Db	1681	TGATCATCAAGAAACTGGAAATTTGTAAAAATTCAAATGTCACAGATCCCAATGTTA	1740
QY	1741	UACAAUAAAAUUGAUAUUGAGCCAUUUCAGUCUUAUUGUCUUAUAGGCCAUUUAAGGCCAA	1800
Db	1741	TACAAATAGATAGAAATTTAGACCATTCACATGCTCCTGATCCTTAGGGCCACAGAAAGCCAA	1800
QY	1801	UACAGUGGGUUUGUUGAGACUCUAUUCCAACAAUAGAGAGUAUUCUGGACAUUUGAU	1860
Db	1801	TACAGCGGTTTGGTAAAGAACCTGTGTTTCACGAAATGGAGATGTACTTGGAAACATTTGAT	1860
QY	1861	ACCAACCCAGUAUAUAAAAUUCUUCUCCUUGAGACGGCCCCACAAAGCAAAAGUAGAUG	1920
Db	1861	ACTGCTCAAAATAAATAAACCTCTCTCTTTGGCGCTGCTCTCCGGAACAGATGAGATG	1920
QY	1921	CAGUUCUCUUCUACUGAGCUGUGAUAUGAGGGGAGUACAGAAUAGAUUAUCUGUAAAGGCG	1980
Db	1921	CAGTTCTCTTCTTGACTGTTAATGTAAAGAGATCGGGAATGAGGATATCTGTAAAGAGCG	1980
QY	1981	AAUUCUCCUAUUAUUCACUAACAACAACCAUAAGAGACUAACAUAUUCUGGGGAAAGAU	2040
Db	1981	AATTCGCCAGTGTCAACTACAAATAAAGCCACTAAAGAGCTCAACAAGTCTTCGGAAAGAT	2040
QY	2041	GCUGGACAUUUAUCUAGAAACCCAGUAAGAGGACAUUCUGGAGUGGAGUCCGUGUUG	2100
Db	2041	GCAAGTGCGCTTACTGAAAGCCAGATGMAAGTACGGCTGGAGTGAATCTTGCTTTCTA	2100
QY	2101	AGAGAUUUCUACAUUCUGGCGAAAGAAUAUGAGAUUAUGACCCAGCAUUAAGCAUCAU	2160
Db	2101	AGAGGGTTTCTCATTTTAGGTAAAGAAACAAAGAGATATGGCCAGCACTAAGCATCAAT	2160
QY	2161	GAACUAGACUAAACUUGGAGAAAGAGAAAGCCUAUUAUACUAUUGGGGCAAGAGACUG	2220
Db	2161	GAATCTGAGCAAACTTTCGAAAGGGGAGAAACCTAATGTGCTAATTTGGGCAAGGGGACCTG	2220
QY	2221	GUGUGUGUAUAGAAACGAAACCGAAACUUCUAGCAUACUACUGACAGCCAGACAGCAGC	2280
Db	2221	GTTGTTGGTAATGAACCGAAACGGAACGTGACTTACGCTACTTACTGACAGCGACAGACGAC	2280
QY	2281	AAAAAGAUUCGGAUGGCCAUCAUAUUAUGUGAAUAGUUUAAAAACGACCUUGCUUUCAC	2340
Db	2281	AAAAGGATTCGATGCGCATCAATTAGTGTGAATGTTTAAAAACGACCTTGTTCAC	2340
QY	2341	U 2341	
Db	2341	T 2341	

RESULT 2  
US-09-506-286B-47  
; Sequence 47, Application US/09506286B  
; Patent No. 6482414



Qy	1801	UACGUGGUGUUNUGUAGACUCUUNUCCAAACAAUAGAGAGUAGUACUUGGACAUUUUAC	1860
Db	1801	TACAGCGGTTTCGTAAAGAACCTGTTTACAGCAAAATGCGAATGTACTTGGAACTTTGAT	1860
Qy	1861	ACCAACCCAGAAUAAUAAAACTUCUUCUUCUUGCAGCCGCCCAACAAAGCAAAAGUAGAU	1920
Db	1861	ACTGCTCAAAATATATAAACTCTCTCTTTCGCGCTGCTCTCTCGGAACAGATAGATG	1920
Qy	1921	CAGUUCUUCUACUCGACUCGUGAUAUGAGGCGAUACGAGAUAGAUACUUCUUGAAGGCGC	1980
Db	1921	CAGTTCTCTTCTTGACTGTTAATGTAAAGAGATCGGGAATGAGGATCTTGTAAAGAGC	1980
Qy	1981	AAUUCUCUAAUUAUACUAACAAAGACCACTAAAGACAUAACAUAUCUUGCAAAAGAU	2040
Db	1981	AATTCGCCAGTGTCTCACTACATTAATTAAGCCACTAAAGAGCTCACAGTCTTGGAAGAA	2040
Qy	2041	GCUGGCAACUUUAACUAGAGACCCAGAUAGAGCAUUCUGGAGUGAGUCCGUGUUCG	2100
Db	2041	CGAGGTGCGCTTACTGAAGACCCAGATAGAGTACGCTGAGATGTAAGATCTGCTGTTCTA	2100
Qy	2101	AGAGAAUUCUACAUUCUCUGGCGCAAAAGAAAGAUAGAGAUUGGACACGACUAUAUACAU	2160
Db	2101	AGAGGGTTTCTCATTTTATGTAAAGAAACAAAGAGATATGGCCGACGACCTAAGATCAAT	2160
Qy	2161	GACACUGAUAACCUUGCGAAAGAGAGAAAGCGUAUUGUACUAUUGGCGCAAGAGACGUG	2220
Db	2161	GAACCTGAGCAAACTTGCAAAAGGGGAGAAAGCTAATGTGCTAATTTGGCAAGGGGACGTG	2220
Qy	2221	GUGUGUGUAUAUAAACGAAAAACGAAACUCUAGCAUAUAUCUAGCAGCGACAAGCGAC	2280
Db	2221	GGTGTTGTAATGAAGAAACGGAACCGTACCTTAGCATACCTTACTGACAGCGACAAGCGACC	2280
Qy	2281	AAAAGAAUUCGGAUUGCGCCAUACUAUUAUUGUGAUAUGUAAAAACGACUCUGUUCUAC	2340
Db	2281	AAAAGATTCGGAATGCGATCCATCAATTAATGTGTGAATTTGTTAAAAACGACCTTGTTTCTAC	2340
Qy	2341	U 2341	
Db	2341	T 2341	
RESULT 3			
US-09-506-286B-46			
Sequence 46, Application US/09506286B			
Patent No. 6482414			
GENERAL INFORMATION:			
APPLICANT: Dowling, Patricia W.			
APPLICANT: Youngner, Julius S.			
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES			
FILE REFERENCE: EO-1-C2			
CURRENT APPLICATION NUMBER: US/09/506,286B			
CURRENT FILING DATE: 2000-02-16			
PRIOR APPLICATION NUMBER: 09/133,921			
PRIOR FILING DATE: 1998-08-13			
PRIOR APPLICATION NUMBER: PCT/US99/18583			
PRIOR FILING DATE: 1999-08-12			
NUMBER OF SEQ ID NOS: 108			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 46			
LENGTH: 2277			
TYPE: DNA			
ORGANISM: Equine influenza virus H3N8			
US-09-506-286B-46			

	Query Match	Score	DB	length
db	Best Local Similarity	66.3%	Pred. No. 0	2277
	Matches 1510;	Conservative 437;	Mismatches 330;	Indels 0; Gaps 0;
Oy	28	AUGGAGAAUAAAGAACUACGGAUUCUGAUGCGCGACUCUCGACUUCGGAGAUACUA	87	
	1	ATGGAGAAATATTAAGAAGCTGAGAGATCTAAAGTGCATACATCCCGACCCGACAGTTACTTA	60	

[illegible]

Db 1021 GAAGAGAGAAATGCTTACGGGCAACTCTTCAAACTTGAATTAAGAGTGCATGAAGGCCTAT 1080

Qy 1108 GAGGAGTUCACAAUGCGTUGGAAAAAGGCAACAGCTUACUCAGAAAAACCAACGAGAGA 1167

Db 1081 GAAGATTTCCAAATGCTGCGAAGAAAGACCAACAGCCTTTCTCAGAAAAGGCAACCGAGAAGA 1140





Db	601	TTGATGTAGTCATACATCTAGTAAAGAGTGGTCCGAAAACAGATTCCTCCCACTG	660
Qy	688	GCUGUGGAAACAAGACUGUGUAUUAUGAUGUUGCAUCUGACUCAAAGAAACAUUGCUG	747
Db	661	GCTGGCGGAAACAAGACAGTGTATCAATTGAAGTTGGTCACTTCGATCTGACGGAAATGCTGG	720
Qy	748	GAAACGAUGUUCACUCCACAGUGUGAACAUGACGAUUGAUGUUGUAUCAAAGUUCUUAU	807
Db	721	GAACAAATGTACACCCACAGAGAGAAAGTTAGAAAACGATGACATTTGATCAAAAGTTAAAT	780
Qy	808	AUUGCAGCGCAGGAGACAUAGUGAGAAAGACAGACGAUUAAGCAGACAUCCAUUCUUA	867
Db	781	ATTGTGCCCCCGGAACAATAGTGAAGAAAGAGACAGATACAGACAGATCCACTAGACCTCGT	840
Qy	868	UUGAGAUUGUCCACACAGACACAGAUUGCGGGACAAGAGUUGUGAACAUUCUUUAAGCAG	927
Db	841	CTGGAATAGTGGCACAGTACACAGATTGGTGGAAATAAGATGGTATGACATCCTTAAGCAG	900
Qy	928	AAACCAACAGAAAGACACAGCUGUGGAAUUAUCCAGCGUGCAUUGGACUACAGAGUCCAGC	987
Db	901	AATCCAAACAGAGAAACAAGCTGTGATTAATCCAAAGACACATGGGCTTAAAGATTAGC	960
Qy	988	UCAUCUCUACUGUUGUGCGGUGUACAUUUAAGAAACAAGCGCAUCCAGUCACAAGAA	1047
Db	961	TCATCATTCACGCTTTGGTGGATTTCACTTTAAGAGAAACAAGTGAATCATCTGCTCAAGGA	1020
Qy	1048	GAGGAGAAGUCCUUAACGCGCAUUCUCAAACAUUGAAAUAUAGGUGUCAUGAGGAAUAC	1107
Db	1021	GAAGAAAGAAATGCTTAAACGGGCAACCTTCAAAATTTGAATAAAGTGCATGAAGGCTAT	1088
Qy	1108	GAGGAGUUCACAUAUGGUGGGGAAAGGGCAACGCUUAUUCAGAAAAGCAACGACGAGA	1167
Db	1081	GAAGAAATTCACAAATGCTCGAAGAAAGACACAGCCATTTCTGAGAAAGCAACAGAAAG	1140
Qy	1168	UUGAUUCCAGCUGAUUUGUGAUGAAAGAGACGAACAGUCGUAUGCUGAACCAUUAUUGUG	1227
Db	1141	TTGATTTCAATTGATAGTAAAGTGGAGAGATGAACAATCAATTCGTGAAGCAATTAATTGTA	1200
Qy	1228	GCCCAUGUAUUTUUCACAAGAAAUUGUAUUAUAAAACGUAUAGUGUGAUCUCAUUC	1287
Db	1201	GCCATGTGGTGTTCGCAAGAAATTTGCAATGAATCAAGACAGTTGCGAGGATTTGCAATTC	1260
Qy	1288	GUUAUAAGGCGAAAUACAGGAGUUGUAUCCACAGCGACUCCAAUCUUUAAGAUAUUCUACAAG	1347
Db	1261	GTTAATAGCAAAATCAGGCGCTTGAACCCCATGCAATCACTTTAGGACATTTCCAAABA	1320
Qy	1348	GAUCCGAAAGUCCTUUTUUCAAAUUUGGGGAAUUGAACAUUACGACAAUUGCAGUUGGAUUG	1407
Db	1321	GATGCAAAAGTCTTTTCCAGAAATGGGGGATTGAACCATGACAAATGTGATGGGAATG	1380
Qy	1408	AUUGGGGUAUUAACAGACAUUACUCCACAGACACAGAGAUUCUCAUGAGGGGUAUAGAUUC	1467
Db	1381	ATTGGAAATATTGCTCGTACATGACCCCAACGACCGAGATGTCAATTTAGAGAGATGTGAGCTC	1440
Qy	1468	AGCAAAAUAGGGGUAUGUAUAUCCACGCGGAGAGAGUAUGUGUGUACGCAUUDACCGG	1527
Db	1441	AGCAAAATGCGAGTGTGATGAGTACTCCAGCACTGAGAGAGTGTGTGACACTTGAACCT	1500
Qy	1528	UUUUUGAGAGUUCGAGACCAACGAGGAAUUGUAUAUAUUCUCCUGACGAGUGCUGUAA	1587
Db	1501	TTTTTAAAGTTCCGGATCAAAAGGGGAAACATATCACTGTCCTCCGAAAGGTCAGTGA	1560
Qy	1588	ACACAGGGAACAAGACAAACUGACAAUAUACUUAUCUACUGUCUAUUGUUGGAGUUAUAU	1647
Db	1561	ACACAGAGAAACGAAAGCTGACAAATTAATTTATCATCAATCATATATGTGGAGATTAAAT	1620
Qy	1648	GGCCUCGAGUCUGUGUGUCUAUAUCCUAUUCAGUGAUCUACCAAAACUGGAAACUGUU	1707
Db	1621	GGTCCCGAATCAAGTGTGGTCAATCTTAATCAATGATCATCAAGAACTGGGAAATTTG	1680
Qy	1708	AAAUUCCAGUGUCUCCAGAUUCCUACAUGCUUAUCAAUAAAUGAAUUTUGAGCCAUUU	1767

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Db      1681  AAAATTCAATGTCACAGATGCCAATGTTATTACAAATAGATAGAAATTTGAGCCATTG 1740
Qy      1768  CAGCTUUUAUUCUCUUAAGGCCAUUAAGGGCCAAUACAGUGUGUUUUUUAAGACUUAUUC 1827
Db      1741  CAGTCCCTGCTGCTCTAGGGCCACAGAAAGCCAAATACAGCGGTTCCTGTAAAGAAACCTGTTT 1800
Qy      1828  CAACAAAUAGAGGAGUAGUCUGGAGACUUDUGAUAACCAAGCAGAUAAUAAACUUCUCCC 1887
Db      1801  CAGCAAAATGCGAGAGTGTACTTGGAACATTGGATTACTGCTCAAAATATAAATCTCTCCCT 1860
Qy      1888  UUUUCAGCCGCCCCCAACCAAGCAAAAGUAGAUAGCAGUUCUUCUACUGACUGAGUAUGUG 1947
Db      1861  TTTGCGCGTCTCTCTCCGGAACAGATAGATGATGATGATGATGATGATGATGATGATGAT 1920
Qy      1948  AGGGGAVUCAGAAUAGAGAUAACTUGUAAGGGGCAUUCUUCUUAUUAUUAACUACAAAG 2007
Db      1921  AGAGGATCGGGAAATGAGAGATTACTGTAAAGAGCAATTCGCCAGTGTCAACTAAATAA 1980
Qy      2008  ACCACUAAGAGACUAAACAAUUCUUGGAAAGAGUGUGGACCUUUAACUAGAACCCAGAU 2067
Db      1981  GCCACTAAGAGGCTCAACAGTCTCTCGAAAGAAAGATGACAGGTGCGCTTACTGAAGACCA 2040
Qy      2068  GAAAGGCACAUUCUGAGUGAGUCCGCTGUCUUCUGAGAGAUUUCUACUUCUGGCAAAAGAA 2127
Db      2041  GAAAGTACGGCTGAGAGTAAATCTGCTGTTCTAAGAGGGTTTCTCATTTTAAGTAAAGAA 2100
Qy      2128  GAUAGGAGUAUUGACACCAAGCAUUAAGCAUACUAGAACUAGUAAACUUGCGAAAGAGAA 2187
Db      2101  AACCAAGAGATATGCGCCAGACACTAATCAATCAATGAGACAAACTTGCCAAAGGGGAG 2160
Qy      2188  AAGGCUAUAUACUAAUUAUUGGGCAAGAGAGUGUGUUAUUAAGAAACGAAACGGAAAC 2247
Db      2161  AAAGCTAATATGCTAATATTGGCAAGGGAGCGTGTGTGTGAATGAACGGAAACGTGAC 2220
Qy      2248  CACGCAUACUUAUCUGACAGCCACAGACACCAAGCAAAAGAUUCGGAUGGCCAUCAU 2304
Db      2221  TCTAGACTACTTACTGACACCGACAGACAGCAACCAAAAGAAATGGCATGCGCATCAAT 2277

RESULT 5
US-09-506-286B-13
: Sequence 13, Application US/09506286B
: Patent No. 6482414
: GENERAL INFORMATION:
:   APPLICANT: Dowling, Patricia W.
:   APPLICANT: Youngner, Julius S.
:   APPLICANT: The University of Pittsburgh, of the Commonwealth
:   TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
:   FILE REFERENCE: EO-1-C2
:   CURRENT APPLICATION NUMBER: US/09/506,286B
:   CURRENT FILING DATE: 2000-02-16
:   PRIOR APPLICATION NUMBER: 09/133,921
:   PRIOR FILING DATE: 1998-08-13
:   PRIOR APPLICATION NUMBER: PCT/US99/18583
:   PRIOR FILING DATE: 1999-08-12
:   NUMBER OF SEQ ID NOS: 108
:   SOFTWARE: PatentIn Ver. 2.1
:   SEQ ID NO 13
:   LENGTH: 1241
:   TYPE: DNA
:   ORGANISM: Equine influenza virus H3N8
:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: (28) ..(1239)
US-09-506-286B-13

Query Match      41.2%; Score 964.2; DB 4; Length 1241;
Best Local Similarity 68.0%; Pred. No. 2,1e-287;
Matches 844; Conservative 224; Mismatches 173; Indels 0; Gaps 0;

Qy      1  AGCGAAAGCGAGUUAUUUAUUAUUGCAUAUUGAAAGAAUUAAGAAACUACGGAUUCGAG 60
Db      1  AGCGAAAGCGAGUUAUUUAUUAUUAUUGCAUAUUGCAUAUUGCAUAUUGCAUAUUGCAUA 60

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QY	481	CGAGACCTCAGUGGCCAAGAGGCAACAGAUUUGAUAUGGAAAGUUGUCCUUAACGA	540
Db	481	CGAGACCTCAGUGGCCAAGAGGCAACAGATGTGATCTAGAAAGTTGTTTCCCAATGA	540
QY	541	GUGGGGGCCAGGUAUCUAACGUCGGAUUCGCAUUAACAAUUAACCAAGAGAAAAAGAA	600
Db	541	GUGGGAGCCAGAAATTTCTAAACATCGGAATCAACAATTAACTCAAAAGAGAAAAAGAA	600
QY	601	GAACTTCAGAGACTGCAAAAATTGCCCCCTTGAATGATGATCAATCTAGAAAAGAGATTG	660
Db	601	GAACTTCAGAGACTGCAAAAATTGCCCCCTTGAATGATGATCAATCTAGAAAAGAGATTG	660
QY	661	GUCCGAAAAACGAGAUUUCUCCAGUGUCUGUGAACAACGAGUGUUAACAUUGAUG	720
Db	661	GUCCGAAAAACAGATTTCTCCCAATGCTGCGGAAACAGCAGATGTATACCTGAACTG	720
QY	721	UUGCACTUGACUCACAAAGAACAUGUCUGGGAAACAGUUAACUCCACGUGGAGAAUGAGG	780
Db	721	TTGCACTGACCTCAGGAAACATGCTGGGAAACAAATGTACACCCCGAGAGAAAGTTAGA	780
QY	781	AAUGAUGAUUGUUAUCAAAGUCUAUUAUUGCAGCCAGAGACUAUGAAGAAAGCAGCA	840
Db	781	AACGATGACATTTGATCAAAAGTTTAATTATTTGCTGCCGGAACATGTAGAAAGCCGACA	840
QY	841	GUUACAGAGANUCCACUAGCUCUUAUUGAGAUUGGCGACAGACACAGUUGGCGGG	900
Db	841	GTATAGCAGATCCACTAGCATCCCTGCTGGAAATGTGCAACATGATCAAGTATGTGTA	900
QY	901	ACAAGAGUUGUGGCAUUCUUAAGGACGAACCCACAGAAAGCAACGUCUGGAAAUAGC	960
Db	901	ATAAGAGATGTGTAGACATCCTTAAGCAGAAATCCACAGAGAAACAAGCTGTGGAATATATGC	960
QY	961	AAAGCUGCAUUGGCACTUGAGAUCAAGCUCUACUCCUUAUGUUGGCGGUCACAUUUAAG	1020
Db	961	AAAGCAGCAATGGGGGTTAAAGAAATTTGATCTCATATTCAGCTTGTGGGATTCACCTTTAAG	1020
QY	1021	AGAAACAACGGGACUACAGUCACAGAGAGAGAGAAAGAUUGCUAAGGGCAUUCUUAACA	1080
Db	1021	AGAAACAAGGTGATCATCACTCAAGAGAGAGAAAGAAATGCTTACGGGCAACTTAAACA	1080
QY	1081	UUGAAAAUAAGGGUCCAGUAGGGAUACGAGAGUUAACAUGUGUUGGCAAAAAGGCAACA	1140
Db	1081	TTGAAATAATGAGGTGCAATGAAGGCTATGAAGAAATTTCAACAATGCTGGAAGAAAGACAA	1140
QY	1141	GCUAUACUCGAAAAAGCAACGAGAGAUUGAUUCAGCUCAGUUGUGGAAAGACAGAA	1200
Db	1141	GCCATTTCTCAGAAAGGCAACCGAAGATGATTCAATTGATGTAGTAAGTGGGAGATGATA	1200
QY	1201	CAGUCGUAUGCUGAAGCAUAUAUUGGCGAUGCUUAUUC	1241
Db	1201	CATCAATTTGCTGAAGCAATTAATTTGAGCCATAGTGTTTTTC	1241

RESULT 7  
US-09-506-286B-16  
; Sequence 16, Application US/09506286B  
; Patent No. 6482414  
; GENERAL INFORMATION:  
; APPLICANT: Dowling, Patricia W.  
; APPLICANT: Youngner, Julius S.  
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES  
; FILE REFERENCE: EQ-1-C2  
; CURRENT APPLICATION NUMBER: US/09/506, 286B  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: 09/133, 921  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: PCT/US99/18583  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: Patentcin Ver. 2.1  
; SEQ ID NO 16

[illegible]



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; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-22

      ery Match      40.2%; Score 941.4; DB 4; Length 1232;
      Best Local Similarity 64.1%; Pred. No. 2.3e-280;
      Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

QY 1111 GAGUUCACAUUGGUGGAAAGGCAACAGCUAUCUCAGAAAGCAACGAGAGAUUG 1170
DB 2 GAATTACACATGTCGGAAGAGAGCAACAGCATTCAGAAAGCAACGAGAGATTGG 61
QY 1171 AUVGAGCUAUGUGAGUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
DB 62 ATTCAATTGATAGTAAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
QY 1231 AUVGAGUAVUUCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
DB 122 ATGGGTGTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
QY 1291 AAUAGGCGCAAUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
DB 182 AATAGAGCAAAATCAGAGGCTTGAACCCCATGATCAACTCTTGAGGCAATTC 241
QY 1351 GCGAAAGUCUUUUUCAAUUGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1410
DB 242 GCAAAAGTCTCTTCCAGAAATTTGGGGATTTGAACCCATCGAACAATTTGATG 301
QY 1411 GGGGUAUUAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1470
DB 302 GGAATATTCCTGACATGACCCCAAGACAGAGATGCTCTTGAAGAGAGAGAGAG 361
QY 1471 AAAAUGGGCGUAUUAUUAUUCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1530
DB 362 AAAATGGGAGTGGATGAGTACTCCAGCACTGAGAGAGAGTGGTGTGAGCAT 421
QY 1531 UUGAGAGUUCGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590
DB 422 TTAAAGATTTGGGATCAAAAGGGGAAACATATCTGTCCCTGAAAGAGTCTG 481
QY 1591 CAGGAGAACAGAGAAACUGACAUAUCUUAUCUUAUCUUAUCUUAUCUUAUCU 1650
DB 482 CAGAGAGACGAGAAAGCTGACATTAATTATTCATCATCATCATATGTGGAGAT 541
QY 1651 CCUGAGUCAGUGUGUGUCAUAUCUUAUCUUAUCUUAUCUUAUCUUAUCUUA 1710
DB 542 CCCGATCATGTTGTGCTCAATCTTATCAATGATCATCAGAGAACTGGGAAAT 601
QY 1711 AUVGAGUUCUUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1770
DB 602 ATTCAATGATGTCACAGAGATCCCAATATTTATCAATTAATTAATTAATTAAT 661
QY 1771 UCUGUAGUUCUUAAGGCAUAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1830
DB 662 TCCCTGCTGCTTGAAGGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
QY 1831 CAAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1890

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DB 722 CAAATGCGAATGATGATCTTGAAACATTTGATGCTCAATAATTAATAATCTCCCTTT 781
QY 1891 GCAGCCGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1950
DB 782 GCGCTGCTCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841
QY 1951 GGAUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2010
DB 842 GGAATCGGAGATGAGAGATGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 901
QY 2011 ACUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2070
DB 902 ACTAAGAGGCTCAAGTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961
QY 2071 GGCACAUUCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2130
DB 962 GGTACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
QY 2131 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2190
DB 1022 AAGGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081
QY 2191 GCUAUAUUAUUAUUGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2250
DB 1082 GCTAATGTGCTAATTTGGGCAAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141
QY 2251 AGCAUAUCUUAUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2310
DB 1142 AGCATCTTACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201
QY 2311 UGAUAGUUUAAAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2341
DB 1202 TGAATTTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1232

RESULT 10
US-09-762-861B-22
; Sequence 22, Application US/09762861B
; Patent No. 6579528
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS (formerly HKZ-033CPUS)
; CURRENT APPLICATION NUMBER: US/09/762,861B
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 22
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-762-861B-22

      Query Match      40.2%; Score 941.4; DB 4; Length 1232;
      Best Local Similarity 64.1%; Pred. No. 2.3e-280;
      Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

QY 1111 GAGUUCACAUUGGUGGAAAGGCAACAGCUAUCUCAGAAAGCAACGAGAGAUUG 1170
DB 2 GAATTACACATGTCGGAAGAGAGCAACAGCATTCAGAAAGCAACGAGAGATTGG 61
QY 1171 AUVGAGCUAUGUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
DB 62 ATTCAATTGATAGTAAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121

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[illegible]

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Db      1202  TGAATTGTTAAAAAGCAGCTTGTTACT 1232
          .:::|:::|||||||:::|:::|:::|:
RESULT 11
US-09-506-286B-19
/ Sequence 19, Application US/09506286B
/ Patent No. 6482414
/ GENERAL INFORMATION:
/ APPLICANT: Dowling, Patricia W.
/ APPLICANT: Younger, Julius S.
/ APPLICANT: The University of Pittsburgh, of the Commonwealth
/ TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
/ FILE REFERENCE: EQ-1-C2
/ CURRENT APPLICATION NUMBER: US/09/506,286B
/ CURRENT FILING DATE: 2000-02-16
/ PRIOR APPLICATION NUMBER: 09/133,921
/ PRIOR FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: PCT/US99/18583
/ PRIOR FILING DATE: 1999-08-12
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 19
/ LENGTH: 1233
/ TYPE: DNA
/ ORGANISM: Equine influenza virus H3N8
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)..(1196)
US-09-506-286B-19

Query Match      40.2%; Score 941.4; DB 4; Length 1233;
Best Local Similarity 64.1%; Pred. No. 2,3e-280;
Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

QY      1111  GAGUUCACAAUUGUGG3AAAAGG3CAACAGCUUACUCACAGAAAAGCAGAGAUUG 11707
DB      3     GAATTTCACAAATGCGCGAGAGAGAACAGCAGCCATTCTCAGAAAAGCAGAACGAAAGTTG 62
QY      1171  AUUAGUGUUAUUGUGAUGGAAAGAGACAGACGUGUGAGUCUGAAGCAUUAUUGGCG 12330
DB      63     ATTCAATGTGATAGTAAGTGGAGAGATGAACATCAATTCGTGAAGCAATATGTTAGCC 122
QY      1231  AUGGUUUUUUCCACAAGAGAAUUGUUAUUGAUAAGAGCUUAGAGUGUUAUUGUGU 12909
DB      123     ATGCTGTTTTCGACAGAAAGATTGCAATATAAAAGCAATTCGAGGCCATTTGAATTCGTT 182
QY      1291  AAUAGGGCAAAUACGCGAUUGAAUUGCCAGUCAUCUUAACUUAUUGUUAAGACAU 13505
DB      183     AATGAGACCAATCAGCGCTTGAAACCCATCATCACTCTTGAGAGCAATTCGAAAAGAT 242
QY      1351  GCGAAAUUGCUUUUUCAAAUUGGGGAUUGAAACUAUUGCACAUAUUGUAGUUGCA 14110
DB      243     GCAAAAGTGTCTTTTCCAGAAATTTGGGGATTGAACCCATCGACAAATGTGATGGGAATGAT 302
QY      1411  GGGGUUAUUCACAGACUAGUACUCCCAAGACAGAGAUUGUCAAUUGAGAGGGGU 14770
DB      303     GGAATATTGCTCTGACATGACCCCAAGACAGCAGATGTCATTGAGAGAGAGTAGAGTACG 362
QY      1471  AAAUUGGCGUAGUGAUAUUCUCCAGGCGGAGAGAGUAGUAGUGUAGACAUUGAC 15310
DB      363     AAATGCGAGTGTGATGATGATCTCCAGCAGTGAAGAGATGCTGAGACATTTGACCGTTT 422
QY      1531  UUGAGAUUUGAGACCAACAGAGAAAUUGUACUUAUUGCUUCCUGAGAGUGUAGU 15909
DB      423     TTAAGAGTTTGGGATTCMAAGGGGAAACATCTACTGCTCCCTGAAAGAGTCACTGA 482
QY      1591  CAGGCAACAGAGAAACUGACAUUAUCUACUUCUGUCAAUUGUGGAGAUUAUUGCC 16550
DB      483     CAGGAAACGGAAGAGCTGACAAATTAATTTATTCATCAATGAATGTGGAGATTAAATG 542
QY      1651  CUGAGUACAGUUGUGUCAAUUAUACUUAUACUUAUACUUAUACUUAUACUUAU 17110
DB      1651  CUGAGUACAGUUGUGUCAAUUAUACUUAUACUUAUACUUAUACUUAUACUUAU

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Db	543	CCCGAATCAGTGTGGTCAATTACTATCAATGATCAATCAGGAACCTGGGAAATTGTGAA	602
Qy	1711	AUUCAGUGUCUCUCAGAAUUCUCAAUUGCUAUACAUAUAAAUUGAAUUTGAGCCAUUCUG	1770
Db	603	ATTCAATGATGTCACAGAGATCCCAATGTTATCAATTAAGATGAAATTGAGCAATCCAG	662
Qy	1771	UCUUUAGUUCUUAAGGCCAUUAGAAGCCAAUUCAGUGGUGUUUGUUGAGACUUAUUCGA	1830
Db	663	TCCCTGGTCCCTTAGGGCCACCAAGAGCCAAATACAGCGGTTTGTAAAGAACCTGTTCAG	722
Qy	1831	CAAAUAGAGGAGUUGACUUGGAGCAUUNUGAUACCAACAGAAUUAUAAACUUCUCCUUCU	1890
Db	723	CAATGTCAGATGTACTTGTGAACATTTGATTACTGCTCAAAATTAATAAACTCCTCCCTTT	782
Qy	1891	GCAGCCGCCCCCAACCAAGCAAAAGUAGAAUUGCAGUUCUCUCUACUGACUGUAGUAGG	1950
Db	783	GCCGCTGCTCCTCCGGAACAGAGTAGAGATGCAAGTTCTTCTTGAACCTGTAAATGAAGA	842
Qy	1951	GGAUACAGAGUAGAAUACUUGUAAUAGGGGCAUUCUCCUAUUAUUCAAUUAACAAGACC	2010
Db	843	GGATCGGGAATGAGGATTACTTGTAAAGAGGCAATCCCAAGTGTTCAACTACAAATAAGCC	902
Qy	2011	ACUAAAGACAUAAACAUUCUGGAAAGAAAGUAGUUGCAGCUUUAUCUAGAAGACCAGUAGA	2070
Db	903	ACTTAAGAGGCTCAGCTACTCTCGAAAGATGCAAGTGAGTGCCCTTACTAAGAACCCAGATGA	962
Qy	2071	GGCACAUCUGGAGUGAGUGCCGUCUGUUCUGAGAGAUUCUUAUUCUUGGCAAAAGAAU	2130
Db	963	GGTACGGCTGGAGTAGAATCTGCTGTCTTAAGAGGGTTCATTAATTTAGTAAAGAAAC	1022
Qy	2131	AGGAGAUUUGACACGACGCAUUAAGCAUUAUUAAGUAACTUAGUAACTUUGCGAAAGAAAG	2190
Db	1023	AAGAAATATGGCCACAGCACTTAAGCAATGAATGAAGAAACTTGCAAAAGGGGAGAA	1082
Qy	2191	GCUAUUGUACUUAUUGGGGCAAGGAGACGUGUGUUGGUUAUUGAAACGAAACGGAACUCU	2250
Db	1083	GCTAATGTCTTAATTTGGGCAAGGAGACGTGTGTTGTATGAAGAAAGAAACGTGACTCT	1142
Qy	2251	AGCAUACUUAUCGACAGCCAGACAGGACCCAAAGAAUUCGAGUUGCCAUCAUUAUUGCU	2310
Db	1143	AGCATACTTAAGTGAAGCCAGACAGGACCAAAAGAAATTCGATGGCCATCAATTAAGTGT	1202
Qy	2311	UGAAUUGUUUAAAAAGCAGCCUGUUGUCUACU	2341
Db	1203	TGAATTGTTTAAAAACGACCTGTGTTCTACT	1233
P<=12			
1-762-861B-19			
-sequence 19, Application US/09762861B			
Patent No. 6579528			
GENERAL INFORMATION:			
APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher			
APPLICANT: Education			
APPLICANT: Downing, Patricia W.			
APPLICANT: Youngner, Julius S.			
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES			
FILE REFERENCE: EO-1-C1-PUS (formerly HK2-033CPUS)			
CURRENT APPLICATION NUMBER: US/09/762, 861B			
CURRENT FILING DATE: 2001-02-13			
PRIOR APPLICATION NUMBER: PCT/US99/18583			
PRIOR FILING DATE: 1999-08-12			
PRIOR APPLICATION NUMBER: 09/133, 921			
PRIOR FILING DATE: 1998-08-13			
NUMBER OF SEQ ID NOS: 43			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 19			
LENGTH: 1233			
TYPE: DNA			
ORGANISM: Equine influenza virus H3N8			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (3)..(1196)			

OTHER INFORMATION:  
US-09-762-861B-19

Query Match	40.2%	Score	941.4	DB 4	Length	1233			
Best Local Similarity	64.1%	Pred. No.	2.3e-280						
Matches	789	Conservative	261	Mismatches	181	Indels	0	Gaps	0

OY	1111	GAGUCUACA	UUGUUGGAAAAGGGGACAGCUA	UUCUGA	AAAGCAACGAGAGAUUG	1170		
Db	3	GAATTCA	CAATGGATCGGAGAGAGCA	CAGCCATTCTC	AGAAAGCAACGAGATGG	62		
OY	1171	AUUCAGC	UGUUGUUGAGUGGAAAGAGACGA	ACAGUCUGA	UGCUGAAACAAUUAUUGUGGCC	1230		
Db	63	ATTCAAT	TGTATAGTAAGTGGAGAGATGA	ATCAATTCATTGCTGAAGCA	TAATATTTGATGACC	122		
OY	1231	AUGGUU	UUUACA	CAAGAUUUUUNAU	AAAAGCAUGUAGAGUGU	UUGAUUUUCGU	1290	
Db	123	ATGGAT	GTGTTTCGAGAGAAATTCAT	AGATPAAAGCGATTGAGGGCA	TTTGAATCTTCGTT	182		
OY	1291	AUUGGG	CAAUUCAGCGCAUUGAAU	UCCCAU	GCACUCAA	CTUUAAGACAUUUUCGAAGAU	1350	
Db	183	AATGAG	CAAAATCAGCGCTTGAA	CCCCATGCATCA	CTTGAGGCATTTCC	CAAAAAGAT	242	
OY	1351	GCGAA	UGCUUUUUUACA	AAUUGGGGAAUUGAA	CAUAUUGACAUUGGAAUUGGGA	AAUUGAU	1410	
Db	243	GCAAA	AGCTCTTTCCAGAA	TTTGGGGATTTGAACCCAT	CACATATGATGATGGGA	ATGAT	302	
OY	1411	GGGUA	UUUACAGACAU	GACUCCACAGACAGAGAU	UUGCAU	GAGAGGGUAGAGUCAGC	1470	
Db	303	GGAA	TATTTGCTGACATGAC	CCCCAGCACCGA	ATGATTCATTGAGAGAGTGA	GAGATCGAC	362	
OY	1471	AAA	UUGGCGUAGAU	GAUUAUUCUCCAGGCGGAGAGAGU	AGUUGGUGAGUUGAC	CCGGUUU	1530	
Db	363	AAAA	TGGAGTGTAGTACTCCAG	ACAGAAAGATGATGATGACATTTGAC	CCGTTT	422		
OY	1531	UUUGAG	UGUCAGACCAACAGAGAAU	UGUACUUAUCUUCUGUAGAGAGU	CAGUGAAACA	1590		
Db	423	TTAA	AGTTCCGGATCA	AAAGGGAAACATATCTG	CCCCGAGAGGTCAGTGA	AAACA	482	
OY	1591	CAGGAA	CAGAGAACTGACAU	AAACUUAUCUACUGUACA	UAGUUGGAGAUUAUUGCC	1650		
Db	483	CAAGAA	ACGGAAAACTGACAA	TATATTTATTCATCA	CAATATGATGGAGATTAA	TGAT	542	
OY	1651	CCUGAG	UCAGUUGUUGUACA	UACCUAUCAGUGUACU	ACAGAAAACUGGAGAAACUGU	UUA	1710	
Db	543	CCCGAT	AGTGGTGGTCA	TACTTATCAATGATCA	TCAGAGAACTGGAAA	TTGTGAA	602	
OY	1711	AUUCAG	UGUUCUACA	UUCUACAUCUUAACA	UUAUAAA	UUGAAUUTUGAGCCAUUU	CAG	1770
Db	603	ATTCA	ATGCTCAGAGATCCCA	CAATGTTTATCAATATGA	ATAGAA	TTTGGAGCCATTC	CAG	662
OY	1771	UCUUU	AGUUCUAAAGGCCAU	UAGAGGCCAAUACAGUGGGUUU	UGUAGACUACA	UUUCCAA	1830	
Db	663	TCCCT	GTGCTCTTAAGGCCCA	CCAGAAAGCCAAATAC	ACGGGTTTCGTA	AGAACCTCTGTT	CAG	722
OY	1831	CAAA	UGAAGGAGUACU	UGGAGCAU	UUGAUACA	CCAGAUUAUAAAA	CUUCUCCUU	1890
Db	723	CAAA	TGCGAGATGATCTTG	AGAACATTTGATCTGCT	CAAAATPATAAA	CTCTCCCTTTT	782	
OY	1891	GCAG	CGGCCCCCA	CCAAAGCAAA	GUAGAUGAGUUCU	UCUACUCAGACU	GUAGUUGAG	1950
Db	783	GCGCG	TGCTCTCCCGAA	CAAGATGAGATGAGTTC	TTCTTTTGAC	GTTPAA	GTGTA	842
OY	1951	GGAU	CAGAGACAAU	ACUUGUAAAGGGGCA	UAUUCUCUUAUUAU	CAACUACA	CAAGACC	2010
Db	843	GGAT	CGGAAATGAGATCTT	GTAAGAGCAATTC	CCAGTGTTC	CAACTA	CAATAAAGCC	902
OY	2011	ACUA	AGACUACA	UAUUCUGGAAAGAGAU	CCUGGCACU	UUUAACUGAAGAC	CCGAGUACA	2070
Db	903	ACTAA	GAGCTCACAGTCTCG	GAAGAGATCAGGTG	CTTACTGTA	AGAACCCAGAT	GA	962
OY	2071	GGCA	CAUUCUGAGU	UGAGUGGCGUCU	UUGAGAGAUUC	CUCAUUCUGGG	CAAGAGAU	2130

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Db      963 GGTACGGCTGAGTAGATCTGCTGTTCTAAGAGGGTTTCTCATTTTAGTAAAGAAAC 1022
Qy      2131 AGGAGAUUAGACCGACGCUUUAAGCAUUAUGAAUCUGAUAACUUUGCGAAAGAGAAAG 2190
Db      1023 AAGAGATATGCGCCAGCACTAAGCATCATATGAATCGAGAACTTGCAAAAGAGGAGAAA 1082
Qy      2191 GGUUAUUGUAUUGGCGAAGAGACGUGUGUUGUUAUUAACGAAAGAGAAACU 2250
Db      1083 GCTAATGTCTAATTTGGGCAAGGGGACGTGTGTGTGAATGAAACGGAAACGTGACTCT 1142
Qy      2251 AGCAUACUUAUGACGACGACGACGACCAAAAGAUUGCGAUGGCGCAUUAUUAUGU 2310
Db      1143 AGCATATCTTACTGACGACGACGACGACCAAAAGATTCGATGCGATCATTAATGTGT 1202
Qy      2311 UGAUAUGUUUUAAAACGACCUUGUUUUCUACU 2341
Db      1203 TGAATTGTTTAAAAAACGACCTTGTCTACT 1233

"UT 13
Sequence 15, Application US/09506286B
Patent No. 6482414
GENERAL INFORMATION:
APPLICANT: Dowling, Patricia W.
APPLICANT: Youngner, Julius S.
TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
FILE REFERENCE: EO-1-C2
CURRENT APPLICATION NUMBER: US/09/506,286B
PRIOR FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: 09/133,921
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/18583
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 1214
TYPE: DNA
ORGANISM: Equine influenza virus H3N8
US-09-506-286B-15

Query Match      40.2%; Score 940.4; DB 4; Length 1214;
Best Local Similarity 68.0%; Pred. No. 4.6e-280;
Matches 825; Conservative 218; Mismatches 171; Indels 0; Gaps 0;

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Db      361 AAATGAAAAGATTAAACACGGAACCTTTGGCCCGCTTATTTTAGAATCAAGTCAAG 420
Qy      448 AUAAGCGGAAAGAGUUGACAUAUAUUCUGUGCAUGACAGACCUUGCAAGGAGGACAG 507
Db      421 ATTAGAGAGAGAGATTGATGTAATTAACCCCTGCTCAGCGGACCTCAGTGCCAAAGAGCA 480
Qy      508 GAUGUAUACUUGGAAGUUGUUUUCUUAACGAAGUGGGGCGCAGAUUAUAUGUGCGAA 567
Db      481 GATGTGATCAATGGAAGTTGTTTCCCAATGAAGTGGAGACGAGAAATCTTAACATCGGA 540
Qy      568 UCGCAUUAUAUAUAACCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 627
Db      541 TCACATCTTAACAAATTAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 600
Qy      628 UUGAUGUGUGUGUACAUUGUUAAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 687
Db      601 TTGATGTGACATATACATGCTGTAAGAAAGAGTTGGTCCGAAAGAAAGAAAGAAAG 660
Qy      688 GCTUGUGGAAACAAAGCAGUGUGUACAUUGAAGUGUGUACAUUGAAGAAAGAAAG 747
Db      661 GCTGGCGGAAACAAAGCAGTGTATCATTTGAAGTGTGATCTGACTCAGGGAACATGCTGG 720
Qy      748 GAACAGAUUUAACUCCAGGUGGAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 807
Db      721 GAACAAATGTACACCCAGAGAGAGAAAGTGAAGAAAGATACATGTATCAAAAGTTTAAT 780
Qy      808 AUUGCAGCCGAGAGCAUAGUGUUAAGAGAGAGCAAGUUAACAGACAGUACUACUUAU 867
Db      781 ATTGCTGCCGGAACATAGTGAAGAGAGAGCAAGTATCAGCAATCATCAGATCCCTG 840
Qy      868 UUGAGAUUGGCAACAGCAGACAGAUUGCGGAGCAAGAGUGUGAUAUUCUAGGAG 927
Db      841 CTGGAATGTGCAACAGTACAGATTTGGTGAATGAATGAATGCTTGAACATCTTAAAGCAG 900
Qy      928 AACCCAAAGAAAGAGCAAGUGUGUUAUAUUGAAGGUCUACUAGGAGAGAGAGAG 987
Db      901 AATCCAAAGAGAGAAACAGTGTGATATATGCAAGAGCAGCAATGAGTGAACATTTAGC 960
Qy      988 UCAUCCUACAUUUGCGGUGUACAUUUAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1047
Db      961 TCATCATTCAGCTTTGGTGGATTCACCTTTAAGAGAAAGAGAGAGAGAGAGAGAG 1020
Qy      1048 GAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1107
Db      1021 GAAGAAGAAATGCTTACGGGCAACCTTCAAAACATTTGAAGATGATGAAGGCTAT 1080
Qy      1108 GAGAGUUAUUAUUGUGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1167
Db      1081 GAAGAATTCACAAATGTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy      1168 UUGAUUACGUGAUUUGUGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1227
Db      1141 TTGATTCATTTGATTAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy      1228 GCCAUGGUAUUCU 1241
Db      1201 GCCATGCTGTTTC 1214

RESULT 14
US-09-762-861B-15
Sequence 15, Application US/09762861B
Patent No. 6579528
GENERAL INFORMATION:
APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
Education
APPLICANT: Dowling, Patricia W.
APPLICANT: Youngner, Julius S.
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
FILE REFERENCE: EO-1-C1-PUS (formerly HKZ-033CUS)
CURRENT APPLICATION NUMBER: US/09/762,861B
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US99/18583

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Db 241 AGGAAGATGCTGGCTCAGACCGCGTAAATGATATCACTTGGCAGTGCATGATGAT 300  
QY 328 AGAAUUGACCAUGACAAGUACGGUUAUUCGAAAUUCCAAAUCUUAUUAUUUGAG 387  
Db 301 AGGAATGACCAACAGACGACCAATTCATTAACAAAAGTCCACAAAACCTAATTTGAA 360  
QY 388 AAAAGUCAAAGUUUAAAACUGAACUUGGCCUUCUUAUUUUAAGAAACCAAGUCAA 447  
Db 361 AAAAGTGAAGATTAAACCGAACCTTGGCCCCCGTTCATTTAGGATCAATCAAG 420  
QY 448 AUAAGCCGAAGUUGACUAAAUCUGGUCAUGCAGACUUCAGUCCCAAGGAGGACAG 507  
Db 421 ATAAAGCGAGAGTTGATGATTAACCTGGGTACGCGAGCTGAGCTCAAGAGACAA 480  
QY 508 GAUUGUAUUGAUGAUGUUUUUCCUUAAGAAUGGCGGCCAGAUACUAAUGUCGAA 567  
Db 481 GATGATCATGGAAGTTGTTTCCCAATGAAGTGGAGCCAGAAATTCMAATCGAA 540  
QY 568 UCGCAUUAUACAUAACCAAGAAAGAAAGAAACUCCAGAGUUGCAAAAUUUCACU 627  
Db 541 TCACAACTAACTAACTAAAGAAAAAGAAAGAACTTCAGAGCTGCAGAAATGCCCC 600  
QY 628 UUGAUGUUGCGUACAUUUAAGAGAGAACUUGUCCGAAAAACGAGAUUUCUCCAGU 687  
Db 601 TTGATGATGACATACCTAGAAAGAGGTTGGTCCAAAAACAAGATTCCTCCAGTG 660  
QY 688 GCUUGUGAAACAAGCAGUUGUACAUGAAGUUGUACUUGACUACAAGAAACUUGCUG 747  
Db 661 GCTGCGGAACAAGCAGTGTATACATTTGAAGTGTGACATCTGACAGGAACATGCTG 720  
QY 748 GAACAGAUUACACUCCAGUGGAGAGAGAAUGAAGUAGUAGUUAUCAAAGUCUAU 807  
Db 721 GAACAAATGTACACCCAGAGAGAGAAAGTTAGAAACGATGACATGATCAAAAGTTAAT 780  
QY 808 AUVGAGCCAGAGCAUUGUAGAGAGAGAGAUUAGAGAUUAGCAUUGCAUUGCAUUCUUA 867  
Db 781 ATTGCTGCCCGGACATGCTGAGAGAGGAGACAGTATCGACAGATCGACATGCAATCCCTG 840  
QY 868 UUGGAGUUGCCACAGACAGACAGAUUGCGCGGACAGAGUUGGACAUUCUUAAGCAG 927  
Db 841 CTGGAATGTGCAACAGTACAGATGTTGGAATTAAGATGTAGACATCTTAAGCAG 900  
QY 928 AACCCAACAAGACCAAGCUGUGAAAUUAGCAAGCUGCAUUGGACUAGAGAUACG 987  
Db 901 AATCCAACAAGAGCAAGCTGTGATATATSCAAACAGCAATGCGGTTAAGAAATTAGC 960  
QY 988 UCAUUCUUCAGUUGGCGGGUUCACAUUUAAGAACAGCGGACUUCAGUCACAGAGA 1047  
Db 961 TCATCATTCAGCTTTGGTGATTCACCTTAAAGAACAGTGTGATCATGATCAAGAGA 1020  
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Db 1021 GAAGAAAGAAATCTTAACGGGCACTTCAACATTTGAAATTAAGTGCATGAAGGCTAT 1080  
QY 1108 GAGGAGUUCACAUGGUGGAAAAAGGCAACGCUUAUCUAGAAAGCAACCAAGAGAGA 1167  
Db 1081 GAAGAAATTCACAAATGTCGAGAGAGAGCAACAGCATTTCTCAGAAAGCAACCAAGAGA 1140  
QY 1168 UUGAUCAGCUGAUGUUGAUGAAGAGACGAACAGUGCAUAGCUGAAAGCAUAUUGUG 1227  
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QY 1228 GCCAUGGUUUUUC 1241  
Db 1201 GCCATGCTGTTTC 1214





QY	1212	AAGAAAGUACACUACAGGAGGCGCAGAGAAAGAACCCGUCACUUGAGUAGAAUAGGAGUAG	180
Db	121	AAGAAATATACATCTAGAGAAAGACAAAGGAAAGAACCCCGCATTTAGGATGAAAGTGAAGAAAG	180
QY	181	GCAGUAGAAAUAVUCCGAGUUAACAGCCGCAAGAGAGAUAAACGAAAUAGUAVUUCUCGAGAGAAAU	240
Db	181	GCAGUAGAAATATCCCAATTACAGCAGATTAAGAGGATTAATGGAAATGATTTCTCGAGAGAAAT	240
QY	241	GAGCAAGGGCAAACTUCUAVGAGAUAAAUAGUGUAGUCCGAGUCCGAGUCCGUGUAGUUA	300
Db	241	GAAACAGGGGCAAAACCTTTGTGAGCAAAACGAAAGATCTGAGCTCAGACCGCGTAAAGTGA	300
QY	301	UACAGUCUCUGUGUACAGUGAGAAUVAAGAAUAGACCAUUGACAAUGUACGUGUACUUVU	360
Db	301	TCACCTCTGAGCAGTGCATGTGTGAAATAGAGATGACCAACAGACGACACATTCATTAT	360
QY	361	CCAAAUAVUACAAAAUUAUUVUUGAGAAAGUCGAAAGGUAUUAACAUUGAACUUVUGC	420
r	361	CCAAAUAGTCTACAAAACCTTATTTGAAAAAGTTGAAAGATTAAACACGGAACTTTGAGC	420
U	421	CCUGUCCAUUUUAGAAACCAAGUCAAUAUACGCGCAAGAGUAGUACUAUAUUCUGUCUAV	480
Db	421	CCGTTCAATTTAGGAAATCAAGTCAGAAATPAGACGAGAGTTGATGTAAACCTGTGATC	480
QY	481	GCAGACUCUACUGUCCAGAGGCGACAGAGUUGUAVUACUAGAAAUUUVUUVUUVUCCUAACGA	540
Db	481	GCGGACCTCAGTCCCAAAAGAGACAAAGATGTGATCATGGAAGTTGTTTCCCAATGGA	540
QY	541	GUGGGAGCCAGAGUACUAAICGUCGAAUCGCGCAUUAUCAAUUAACCAAGAGAAAAAGAA	600
Db	541	GTGGGAGCCAGAAATTTCAATCTCGGAATCAACCTAAACATTAACCAAGAGAAAAAGAA	600
QY	601	GAAUUCACAGAUUGCAAAAUUUCACUUVUAGUGUGUGUAGUAGUAGUAGAGAGAAU	660
Db	601	GAACTTCAGAGACTGCAGAAATTCGCCCTTGATGTAGCATACATGCTAGAAAGAGGTTG	660
QY	661	GUCCGAAAAACAGAUUVUUCGCCAGUGUGUGUGAGAACAGAGUUGUUAUUVUAGUG	720
Db	661	GTCCGAAAAACAAAGATTTCTCCCAAGTGTGCGGAGAACAGCAGTGTATCATTTGAAAGTG	720
QY	721	UUGCAGUCUACUICAGAGAAACUUCUGUGGAAACAAUUVUACUUCACAGUGAGAAAGUAGG	780
Db	721	TTGCATCTGACCTCAGAGGAAACATGCTGAGAAACAAATGTACACCCACAGAGAGAAAGTTGA	780
QY	781	AAGUAGUAGUUGUACAAAGUCUUAUUVUAGCAGCCAGAGAGCAUAGUGAGAGAGCAGCA	840
Db	781	AACGATCAGATTGATCAAAAGTTTAAATTGTCCTGCCGAGAACATATGTAGAAACAGGACAC	840
QY	841	GUUACAGCAGUUCACUAGUACUUCUUAUUGAGAGUGGCCACGACACACAGUUGCGGG	900
Db	841	GTATCAGCAGATCCATACATCCCTGCTGGAATGTGCCACAGTACACAGATTTGATGTGA	900
QY	901	ACAAAGAUUGGAGACUUVUUGGCGAGAAACCCAAACGAAAGAGACUGUGGAAUUAUUC	960
Db	901	ATAAGATGTATGACATCTTAAAGCAGAAATCCAAACAGAGAACAGCTGTGGATATATGC	960
QY	961	AAGGUCGCAUUGGAGCUGAGAGUACAGUCUACUUCUUCAGUUVUUGGCGGUGUACAUUUAAG	1020
Db	961	AAAGCAGCAATGGGGTTTAAAGAAATTACCTCATTTGCTTGTGTGATTCACCTTTAAG	1020
QY	1021	AGAACAGCGGCAUUCACUACAGAGAGAGAAAGAAUGUCUUAACGGGCAUUCUUCAAAAC	1080
Db	1021	AGAACAGGTGATCATCTAGTCAAGAGAAAGAAATGCTTACGGGCAACCTTCAAACA	1080
QY	1081	UUGAAAAUVAAGGUGCAGAGGAGUACGAGAGUUCGAAUGUUGGUGGAAAGGCGACACA	1140
Db	1081	TTGAAAAATTAAGATGATGAAGGCTATGAAAGATTCAACAATGATGCGAAGAACAGCACACA	1140
QY	1141	GCUAUACUACAGAAAGCAACAGAGAGUAGUUCAGUCUAVUUGUAGUGAGAGACAGCAA	1200
Db	1141	GCATTTCTCAGAAAGCAACAGAAAGATGTCAATTTGATTAAGTGTGAGAGAGATGAA	1200

QY	1201	CAGUCGUAAGUCGUAAGCAUAUAUUGUGCCAUUGSUUAUUCACAAGAAAGUAUUGUAUAU	1260
Db	1201	CAATCAATTGCTGAAGCAAMTAATTGTAGCCATGCTTTGCGAAGAAAGATTGCATGATA	1260
QY	1261	AAAGCAGUUAAGGUGUAUUCGUAAUUGUGGCAUAUAGGGCAUAUAGCGAUUAUCCCAUG	1320
Db	1261	AAAGCAGTTGAGGCGGATTTAACTTGCTTTATATAGCAAAATCAGCGCTTGMACCCTATG	1320
QY	1321	CAUACAUCUUUUAAGACAUUUUCAGAAAGAUUGCGAAAGUGCCUUUUCAAAUUGGGGGAUU	1380
Db	1321	CATCAACACTTGAAGGACATTTCCAAAAGATGCAAAAAGTGCTTTTCCAGATTTGGGGGATTT	1380
QY	1361	GAACUAUAUCCGACAUAUGUAUGGGGAUAUAUUGGGGUUAUATCCAGACATGACUCCAAAGACA	1440
Db	1361	GAACCCCATTCGACAAATGTGAATGGGAATATATTTGCAATATTCGCTGACAAAGCCCCAAGACC	1440
QY	1441	GAGAUUUCUAUAGAGAGGGGUAAAGUACAGCAAAAUGGGCGGUAGUAUAUUCUCCAGGCGG	1500
Db	1441	GAGATGTCTATTGAGAGAGATGATAGAGTACGCAAAAATGGGAATGATATGATCTCGAGACT	1500
QY	1501	GAGAGAGUAGUGUGAGGACAUUGAACCGGUAUUGAGAUUUCGAGACCAAGAGAAUAUGUA	1560
Db	1501	GAGAGAGTGGTGGTGAAGATTAACCGTTTAAAGATTTGGGATTCAAAGGGGAAACATA	1560
QY	1561	CUACUAUUCUCCUGAGAGAGUGUCAGUAAAACAGGGAAACAGAAACUAGCAUAUAUCUAC	1620
Db	1561	CTACTGTCCTCCCTGAAGGTCAGTGAAGAAACCAAGAGAAACGAAAAAGCTGACAAATATTTAT	1620
QY	1621	UCAUUCUCAAUAUGUGUGAGUAUAUAGCCUUGAGUACAGUUGUUAUUAUACUUAUCAG	1680
Db	1621	TCATCATCAAAAGATGTGGAGATTTAAATGTGCCGAATACAGTGTGGTCAATATCTTATCBA	1680
QY	1681	UGGUAUACAAGAAACUGGGGAAAACUGUUAUUUAUUCAGUGUGUUCGAAUUCUACUAUCUA	1740
Db	1681	TGATATCATCAGAAACTGGGAAATGTGAAAATTTCAATGTCTACAGATCTCCACAAATGTTA	1740
QY	1741	UACAAUAAAUAUGAAUUNUGAGCCCAUUCAGUCUUUAUCUUAAGGCCAUUUGAGGCCAA	1800
Db	1741	TACATAATAGATAGAAATTTGAGGCCATTCAGTCCCTGTGCTCCCTAGGGCCACACAGAAAGCCAA	1800
QY	1801	UACAGUGGUGUUUGUAAGCAUCUUAUUCCAAAUUGAGGGAUGUAUCUUGGGAUAUUGAU	1860
Db	1801	TACAGCGGTTTCTGTAAGAACCTCTGTTTCAGCAAAATGCGAGATGTACTTGGAAACATTTGAT	1860
QY	1861	ACCAACCCAGUAUAUAAAACUUCUUCUCCUUGCAGACCCGCCCAACCAAGCAAAAGUAUAUG	1920
Db	1861	ACTGCTCAAAATATATAAACTCTCTCCCTTTTTCGCGCTGCTCTCCGGAACAGATGAGATG	1920
QY	1921	CAGUUCUCUACUGACUGACUGUAUAUGAGGAGGAGUACAGAAUAGAUUAUCUUGUAAGGGC	1980
Db	1921	CAGTCTCTCTTCTTGACTGTAAATGTAAAGAGATCGGGAATGAGAGATATCTTGTAAAGGCG	1980
QY	1961	AAUUCUCUUAUAUUCACUAACAACAACACCUAAGAGACUAACAUAUUCUCUGGAAAGAAU	2040
Db	1961	AATTCGCCAGGTTTCAATCTACAAATPAAAGCCACTAAGAGGCTCAACAAGTCTTCGGAAGAGAT	2040
QY	2041	GUUGGCAUUUAUCUAAAGCCAGUAUGAGGCAUAUCUGGAGUGAGUUCGCGUGUUCG	2100
Db	2041	GAGGTGCGCTTACTGAAAGACCCAGATGATAGATCTCGCTGAGATGAAATCTGCTGTTCTA	2100
QY	2101	AGAGGAUUCUUCUAUUCUGGCGCAAGAGAGUAUGAGAUUAUGGACCGACGAUAUAAGCAUAU	2160
Db	2101	AGAGGGTTTCTCATTTTATGTAAAGAAACAAAGAGATATGGCCGACGACTAAGCATCAAT	2160
QY	2161	GAACUAGUAUAACUUGCGAAAGAGAAAGGCUAUAUGUAUAUUGGGCAAGAGAGUG	2220
Db	2161	GAACGTGACAAACTTTGCAAAAAGGGGAGAAAGCTAATGTGCTAATTTGGGCAAGGGGACCTG	2220
QY	2221	GUUGUUGUAUAUGAAACGAAACCGAAACUUAUGCAUAUCUAUUGCAGCGACACAGCGACAC	2280
Db	2221	GTTTGTGTAATGAAACGGAAACGATGACTTATGCACTTACTTGACAGCGCAACAGCGCAC	2280
QY	2281	AAAAGAUUCGGAUUGCCCAUCAAUAUUAUGUUGAAUAGUUUUAACCAACCUUGUUUCUAC	2340



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QY 1621 UCAUCGUCACUAGUUGGAGAUUAUGGCCUGGAGUCAGUGUCGUCACUAUCCUAUCAG 1680
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1621 TCATCATATGATGAGGAGATTAATGATCCGAAATCAGTGTGTCAATCACTTATCA 1680
QY 1681 UGAGCAUCAGAAACUGGAAACUGUUAUAUUCAGUGUCUACAUAUCUAUUGUA 1740
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1681 TGGATCATCAGAACTGGGAAATGTGAAATTCATGATGTCACAGATCCCAATGTTA 1740
QY 1741 UCAUUAUUAUUGAAUUVUGAGCCAUUCAGUCUUAUUGUCUAAGGCCAUUUGAGCCAA 1800
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1741 TACAAATAGATAGATTTTGAATTCAGATTCAGTCCCTGCTCCCTAGGCCACAGAGCCAA 1800
QY 1801 UACAGUGGUGUUGUUGAGUCUCUAUUCGAAACAAUAGAGAGUUAUCUUGAGCAUUGAU 1860
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1801 TACACGCGTGTGTAAGAACCTGTTTCAGCAATTCGAGATGTACTTGGAACATTTGAT 1860
QY 1861 ACCACCCAGUUAUUAUUAUUCUUCUUGAGCCGCCCAACCAAGCAUUAUUGAU 1920
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1861 ACTGCTCAATATATAAACTCTCTTTCCTTTCCTGCTCTCCGAAACAGATGAGATG 1920
QY 1921 CAGUCUCUCUACUCAGUCGUAUUGAGGAGUAGAGAAUUAUAGGAG 1980
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1921 CAGTCTCTCTTTCATTTTGAATTTGAAGAGATCGGAAATGAGATCTTTGAAGAGG 1980
QY 1981 AAUUCUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2040
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1981 AATTCCTCCAGTGTTCATCAATTAAGGCACTAAGAGGCTCAGATCCTCGGAAAGAT 2040
QY 2041 GUGGACACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2100
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2041 GAGGATGCGCTTACGAAACCCAGATGAGAGGTACGCTGAGTGAATCTGCTGTTCTA 2100
QY 2101 AGAGAAUUCUCUACUCGAGCAAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2101 AGAGGTTTCTCATTTTGAATTTGAAGAAACAAAGATATAGGCCAGCACTAAGCAAT 2160
QY 2161 GAACTGAGCAAACTTGCAAAAGAGGAGAAAGCTAATGTCTAATTTGGGCAAGGAGCCTG 2220
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2161 GAACTGAGCAAACTTGCAAAAGAGGAGAAAGCTAATGTCTAATTTGGGCAAGGAGCCTG 2220
QY 2221 GUGUGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2280
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2221 GUGUGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2280
QY 2281 AAAAGAUUCGAGUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2340
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2281 AAAAGAUUCGAGUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2340
QY 2341 U 2341
DB 2341 T 2341

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RESULT 3  
US-10-065-133A-46

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; Sequence 46, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 2277

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; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; US-10-065-133A-46
Query Match      74.7%; Score 1749; DB 13; Length 2277;
Best Local Similarity 66.3%; Pred. No. 0;
Matches 1510; Conservative 437; Mismatches 330; Indels 0; Gaps 0;

QY 28 AUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 87
DB 1 ATGAGAGAAATTAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 60
QY 88 ACAAACCCAGAGGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 147
DB 61 ACAAACCCAGAGGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 120
QY 148 AAGAACCCGAGCCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207
DB 121 AAGAACCCGAGCCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 208 AAGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 267
DB 181 AAGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 240
QY 268 AUGAGUAGUAGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 327
DB 241 ACGAACCATCTGCTCAGACCCGCTAATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 328 AGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 387
DB 301 AAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 360
QY 388 AAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 447
DB 361 AAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 420
QY 448 AUAAGGAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 507
DB 421 AUAAGGAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480
QY 508 GAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 567
DB 481 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 568 UCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 627
DB 541 TCACAACTAATTAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600
QY 628 UUGAGUUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 687
DB 601 TTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 688 GUGUGUGAAACAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 747
DB 661 GCTGCGGAAACAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 720
QY 748 GAACAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 807
DB 721 GAACAAATTAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 780
QY 808 AUUCGAGCCAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 867
DB 781 ATTGCTCCCGGAAACAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 840
QY 868 UUGAGUUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 927
DB 841 CTGGAATGTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 928 AACCAACAGAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 987
DB 901 AATCAACAGAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 960
QY 988 UCAUCUCUAGUUGGCGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1047

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Db      961 TATATCTTACGCTTGGTATTCACCTTTAAGAGAAACAGTGGATCATCAGTCAAGAGA 1020
Qy      1048 GAGAAAGAAUGUCUUAACGCGCAUUCUUAACAUTGAAAAUUAAGGUGCAUGAGGAAUAC 1107
Db      1021 GAAAGAAATATGCTTAACGGGCAACCTTCAAAACATTAATAAGATGATGAAGGCTAT 1080
Qy      1108 GAGAGAUUCAUAGUGUUGGAAAAAGGCAACGCTUUAUCUAGAAAGCAACGAGAGA 1167
Db      1081 GAAGAATTCACATATGCTCGAAGAGAGCAACGCAATTCCTCGAAGAGCAACGAGAGA 1140
Qy      1168 UUGAUUACGUGUUGUGUGGAGAGAGCAACAGUCGUAUGUGAGCAUUAUATGUG 1227
Db      1141 TTGATTCATTTGATAGTGGAGAGAGATGAACATATGCTGAGACCAATTAATTGTA 1200
Qy      1228 GCCAUGUUAUUCUACAAGAGAUUGUUAUAAAAGCAUUAAGAGUAGUUCUGAAUUC 1287
Db      1201 GCCATGCTGTTTTCGAGAGAAAGATTGCATGATTAAGAGAGTTGAGGCAATTC 1260
Qy      1288 GUUAUAGGCGCAAUACGCGAUUGAAUCCCAUGCAUAACTUUUAAGCAUUCUAGAG 1347
Db      1261 GTTAATAGAGCAAAATCAGCGCTTGAACCCATGCAATCACTTGGAGCATTCGAAAA 1320
Qy      1348 GAUGGAAAGUGUCUUUUAACAAUUGGGAUUGAUCGUAUGAGUUGGGAUUG 1407
Db      1321 GATGCAAAAGTGTCTTTCCAGAAATTTGGGAGATTGAACCATGACACATGTATGAGAAATG 1380
Qy      1408 AUUGGGGUUAUUAACAGACAUAGACUCCAGACACAGAGAUUGCAUAGAGGGGUAAAGUC 1467
Db      1381 ATTGGAATTTGCTCTCAATGACCCCAAGACCGAGATGTCATTTGAGAGAGTGAAGTTC 1440
Qy      1468 ACCAAAUUGGCGCUAGAUAGAAUUCUCACGCGGAGAGAGUAGUGUGAGCAUUAACCG 1527
Db      1441 AGCAAAATGGAGTGTAGTATGACTCTCAGACATGAGAGAGTGTGTAGATTCAGCCGT 1500
Qy      1528 UUUUUGAGAGUUGAGAACCAAGAGAGAAUUGUACUUAUCUCUGGAGAGAGUGUA 1587
Db      1501 TTTTAAAGAGTTCTGGGATCAAAAGGGGAAACATATCTCTCTCCCTGAAAGTTCAGTGA 1560
Qy      1588 ACACAGGGAACAGAGAAACUGACAAUUAACUACUACUACUACUAGUUGGAGAUUAU 1647
Db      1561 ACACAGGAAACGGAAGAAAGCTGACAAATTAATTTATCTATCTATGATGTGGAGATTAT 1620
Qy      1648 GGCCTCUGAGUAGUUGUUGCAUUAACUUAUCAGUGUAGUAGAAACUGGAAACUGU 1707
Db      1621 GGTCCGGAATCAGTGTTCATTAATCTATCATATGATCATCAGGAATCGGAAATTTGTG 1680
Qy      1708 AAAAUUCAGUGUCUCAGAAUUCUACAUUGUACAUAAAUUGAAUUAUUGAGCCAUU 1767
Db      1681 AAAATTCAAATGTGTCAACAGATCCCAATGTATATACAAATAGATAGAAATTTGAGCATTC 1740
Qy      1768 CAGUCUUUAGUUCUUAAGCCAUUAGAGCCAAUUAAGUGGUGUUGUUGAGCUCUUAUUC 1827
Db      1741 CAGTCCCTGTCTTACGAGCCACACAGAGCCAAATAGCGGTTTGTGAAGAACCTGTTC 1800
Qy      1828 CAACAAUAGAGGAGUAGUUCUGGAGCAUUGUUAUACCAACCCAGAUUAUUAACUUCUCC 1887
Db      1801 CAGCAAAATGCGAGATGTACTTGGAACTTTGATACGTCTCAATATAATAAACTCTCCCT 1860
Qy      1888 UUUUGACCGCCGCCACCAAAAGCAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1947
Db      1861 TTTTCCGCTGCTCTCCGAAACAGATAGATGAGTCTCTTCTTTGCTTTATATTA 1920
Qy      1948 AGGGAGUACGAAUAGAAUUAUCUUGAAGGGCAUUAUUGCUUAUUAUUAUUAUUAUUA 2007
Db      1921 AAGAGATTCGGAATGAGATTAATTAAGAGGAAATTTCCCAAGTTTCAATCAATAA 1980
Qy      2008 ACCACUAGAGCUAAUUAUUCUGGAGAGAGAGUAGUAGUAGUAGUAGUAGUAGUAGU 2067
Db      1981 GGCACATTAAGAGGCTCACTCTCCGAAAGAGATGCGAGTGGCGCTTAAGTAACCAAGAT 2040
Qy      2068 GAAGCAGACUUCUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 2127
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Db      2041 GAAGTACGCGCTGAGATGAATCTGCTGTTCTAAGAGGTTTCTCATTTTAAAGAA 2100
Qy      2128 GAUUGAGAUUUGAGACGACGCAUUAAGCAUUAAGCAUUAAGCAUUAAGCAUUAAGCA 2187
Db      2101 AAGAGAGATATGCGCCGACGACTAAGCATCAATGAATGAGCAAACTTGGAAAAAGGAG 2160
Qy      2188 AAGCUAAUUGAUCUUAUUGGCGCAAGAGAGAGUGUGUUGUUAUUAUUAUUAUUAUUA 2247
Db      2161 AAAGCTAATGTGCTAATTTGGGCAAGGAGAGCGTGTGTGTGTATGAAGAAACGAGAC 2220
Qy      2248 UCUGACUACUUAUCGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2304
Db      2221 TCTAGCTACTTACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2277

RESULT 4
US-10-065-133A-49
; Sequence: 49; Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 49
; LENGTH: 2277
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-49

Query Match      74.5%; Score 1744.2; DB 13; Length 2277;
Best Local Similarity 66.2%; Pred. No. 0;
Matches 1508; Conservative 436; Mismatches 333; Indels 0; Gaps 0;

Qy      28 AUGAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 87
Db      1 ATGAGAGAAATTAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 60
Qy      88 ACAAACCCAGAGGACCAUUAUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 147
Db      61 ACAAACCCAGAGGACCAUUAUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 120
Qy      148 AAGAACCCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 207
Db      121 AAGAACCCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 180
Qy      208 AAGAGAUUAACAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 267
Db      181 AAGAGATTAATGAAATGATTTCTGAGAGAAATGAACAGAGGCAAACTTTGAGAGAA 240
Qy      268 AUGAGUAGUCCGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 327
Db      241 ACGAAGCATGTGCTGAGACCGGCTGAATGTATCACTCTGCGAGATGATGTGAAAT 300
Qy      328 AGAAACCCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 387
Db      301 AGAATGAGACCAACAGAGACGACCAATTCATTAATCCAAAGTCCACAAATCTATTGGA 360
Qy      388 AAGACUCAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 447
Db      361 AAAGTTGAAGATTAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 420
Qy      448 AUAAGCGGAAAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 507
Db      421 ATAAGACGAGAGATTTGATTAACCCCTGTGTACGCGGAGACCTCAGTGCACAAAGACAA 480
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[illegible]

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OY 1588 ACACAGGGAACAGAGAAACUGAACAUUACUUAACUUAACUGACACGACAAAGAGAGUGAGAGAUUAAU 1647
Db 1561 ACACAGGGAACAGAGAAACUGAACAUUACUUAACUUAACUGACACGACAAAGAGAGUGAGAGAUUAAU 1647
OY 1648 GGCCTCUGAGUGCUGAGUGUGUCCAUAUUCGUGAGUACUACAGAAAACUGGAAAACUGUU 1707
Db 1621 GGTCCCGAATCAGTGTGTCAATTAATTATCAATGATCATCAGGAACCTGGAAATTTGTG 1680
OY 1708 AAAAUUCAGUGUCUCUGAAUUCUACAUUCGUACAUUAAAUAUGAAUUBUUGAACCCAUU 1767
Db 1681 AAAATTCAATGTGTCAACAGATCCCAAAATTGTATACAAATGAATGAATTTGAGACCAATTC 1740
OY 1768 CAGUCUUGUUCUUAAGGCAUUAAGGCAUAUAGGCGCAUAUCGUGGUGUUUGUUAACUCUUAUUC 1827
Db 1741 CAGTCCCTGTGCTCTTAGAGGCCACCAAGAGCCAAATACACGCGTTCGTAAAGAACCTGTGTT 1800
OY 1828 CAACAAUUGAGAGGAGUUAUCUUGGACAUUUGAUUACCAACCCAGAUUAUAAAACUUCUCC 1887
Db 1801 CAGCAAAATGCGAATGTACTTGGAAACATTTGATATCTGCTCAAAATATATAAATCTCTCCCT 1866
OY 1888 UUTUGCAGCCGCCCAACAAAGCAAAAGUAGAUUGCAUUCUUCUUCACUGACUGUGAUUGUG 1947
Db 1861 TTTCGCCCTGCTCTCCGGAACAGAGATGAGATGCAGTTCTTCTTGACGTGTAATGTA 1920
OY 1948 AGGGGAUACAGAAUUGAAUAUACUUGUAAAGGGCAUUCUUCUUAUUAUUAACUACUACAG 2007
Db 1921 AGAGGAATCGGAAATGAGAGAAATCTTTGAAGAGGCAATTTCCCAAGTTCUACATCAATPAA 1980
OY 2008 ACCAUAUAGAGCUAAUAUUCUUGGAAAGAGAUUGCUGGACAUUUAACUGAAGACCCAGAU 2067
Db 1981 GCCACTAAGAGCTCACAGATCTCTGGAAAGATGCAAGTGGCGCTTACTGAAGACCAAT 2040
OY 2068 GAAAGCAUUCUGGAGUGAGUCCGCGUGUUCUGAGAGAUUCUUCUUCUGGSCAAAGAA 2127
Db 2041 GAAAGTACCGGTGAGTAGAAATCTGCTGTCTAAGAGGCGTTTCTCATTTTGTAGTAAAGAA 2100
OY 2128 GAUUGAGAUUUGAACCCAGCAUUAAGCAUUAACUAGAUUACUUGCAAAAGAGAA 2187
Db 2101 AACCAAGATATGTGCGCCAGCACTAAGCATTAATTAACCTGAGCAAACTTGCAAAAGGGAG 2166
OY 2188 AAGCUAAUUGUACUAAUUGGCAAGAGAGACGUGUGUUGUGUAUGAAACGAAACGCAAC 2247
Db 2161 AAGCTAATATGTCTAATTTGGGCAAGGGGACGTGGTGTGGTATGMAAGCAAAACGTGAC 2220
OY 2248 UCUAGCAUACUUAACUAGCAGCAGCAGACGACCAAAAGAGUUCGAGUCCAUCAU 2304
Db 2221 TCTAGCAATACTTAACGACAGCCACAGCCAAAGGAAATTCGATGGCCATCAAT 2277

RESULT 5
US-10-065-133A-13
: Sequence 13, Application US/10065133A
: Publication No. US20030199074A1
: GENERAL INFORMATION:
: APPLICANT: Dowling, Patricia W.
: APPLICANT: Youngner, Julius S.
: TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
: FILE REFERENCE: EO-1-C2-1
: CURRENT APPLICATION NUMBER: US/10/065.133A
: CURRENT FILING DATE: 2002-12-10
: PRIOR APPLICATION NUMBER: PCT/US99/18583
: PRIOR FILING DATE: 1999-08-12
: PRIOR APPLICATION NUMBER: 09/133,921
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 108
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 13
: LENGTH: 1241
: TYPE: DNA
: ORGANISM: Equine influenza virus H3N8
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (28)..(1239)

```

## OTHER INFORMATION:

US-10-065-133A-13

41.2%; Score 964.2; DB 13; Length 1241;

Query Match Best Local Similarity 68.0%; Pred. No. 1.8e-268; Matches 844; Conservative 224; Mismatches 173; Indels 0; Gaps 0;

QY 1 AGCGAAGCGAGUCUUAUUUUCUAUUGGAAAGAAUUAAGACUAACGAAUUCUGAUG 60  
 DB 1 AGCGAAGCGAGUCUUAUUUUCUAUUGGAAAGAAUUAAGACUAACGAAUUCUGAUG 60  
 QY 61 UCGAGUCUGGCAUUCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120  
 DB 61 UCGAGUCUGGCAUUCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120  
 QY 121 AAGAAGUACAUUGAGGAGGACAGAGAAAGAACCCGUCACUUGAGUAGUAGUAGUAGU 180  
 DB 121 AAGAAGUACAUUGAGGAGGACAGAGAAAGAACCCGUCACUUGAGUAGUAGUAGUAGU 180  
 QY 121 AAGAAGUACAUUGAGGAGGACAGAGAAAGAACCCGUCACUUGAGUAGUAGUAGUAGU 180  
 DB 121 AAGAAGUACAUUGAGGAGGACAGAGAAAGAACCCGUCACUUGAGUAGUAGUAGUAGU 180  
 QY 181 GCAUUGAAUUAUUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 240  
 DB 181 GCAUUGAAUUAUUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 240  
 QY 181 GCAUUGAAUUAUUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 240  
 DB 181 GCAUUGAAUUAUUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 240  
 QY 241 GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300  
 DB 241 GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300  
 QY 241 GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300  
 DB 241 GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300  
 QY 301 UCAACUCUGGCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360  
 DB 301 UCAACUCUGGCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360  
 QY 301 UCAACUCUGGCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360  
 DB 301 UCAACUCUGGCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360  
 QY 361 CCAAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 420  
 DB 361 CCAAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 420  
 QY 361 CCAAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 420  
 DB 361 CCAAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 420  
 QY 421 CCUGUCCAUUUUUGAAACCAAGUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480  
 DB 421 CCUGUCCAUUUUUGAAACCAAGUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480  
 QY 421 CCUGUCCAUUUUUGAAACCAAGUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480  
 DB 421 CCUGUCCAUUUUUGAAACCAAGUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 480  
 QY 481 GCAGACCCUAGUCGCAAGAGAGGACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 540  
 DB 481 GCAGACCCUAGUCGCAAGAGAGGACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 540  
 QY 481 GCAGACCCUAGUCGCAAGAGAGGACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 540  
 DB 481 GCAGACCCUAGUCGCAAGAGAGGACAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 540  
 QY 541 GUGGAGGCGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600  
 DB 541 GUGGAGGCGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600  
 QY 541 GUGGAGGCGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600  
 DB 541 GUGGAGGCGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 600  
 QY 601 GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 660  
 DB 601 GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 660  
 QY 601 GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 660  
 DB 601 GAACUCCAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 660  
 QY 661 GUCCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 720  
 DB 661 GUCCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 720  
 QY 661 GUCCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 720  
 DB 661 GUCCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 720  
 QY 721 UUCGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 780  
 DB 721 UUCGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 780  
 QY 721 UUCGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 780  
 DB 721 UUCGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 780  
 QY 781 AANAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 840  
 DB 781 AANAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 840  
 QY 781 AANAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 840  
 DB 781 AANAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 840  
 QY 841 GUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 900  
 DB 841 GUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 900  
 QY 841 GUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 900  
 DB 841 GUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 900  
 QY 901 ACAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 DB 901 ACAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 QY 901 ACAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 DB 901 ACAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 960  
 QY 961 AAGGCUCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1020  
 DB 961 AAGGCUCAUUGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1020

DB 961 AAGAAGCAATGGGCTTAAGATTAGCTCATTCAGCTTGTGAGATTCACCTTTAAG 1020  
 QY 1021 AAGAAGCAATGGGCTTAAGATTAGCTCATTCAGCTTGTGAGATTCACCTTTAAG 1080  
 DB 1021 AAGAAGCAATGGGCTTAAGATTAGCTCATTCAGCTTGTGAGATTCACCTTTAAG 1080  
 QY 1081 UUGAAAUUAAGGUCUUAUGAGGAAUACAGAGAGUUAUUAUUAUUAUUAUUAUUAU 1140  
 DB 1081 UUGAAAUUAAGGUCUUAUGAGGAAUACAGAGAGUUAUUAUUAUUAUUAUUAUUAU 1140  
 QY 1141 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1200  
 DB 1141 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1200  
 QY 1201 CAGUCGUAUGCUAAGAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1241  
 DB 1201 CAGUCGUAUGCUAAGAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1241

## RESULT 6

US-10-065-133A-16

Sequence 16, Application US/10065133A

Publication No. US2003019074A1

GENERAL INFORMATION:

APPLICANT: Dowling, Patricia W.

APPLICANT: Youngner, Julius S.

TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES

FILE REFERENCE: EQ-1-C2-1

CURRENT APPLICATION NUMBER: US/10/065, 133A

PRIOR FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: PCT/US99/18583

PRIOR FILING DATE: 1999-08-12

PRIOR APPLICATION NUMBER: 09/133,921

NUMBER OF SEQ ID NOS: 108

SOFTWARE: PatentIn version 3.1

SEQ ID NO 16

LENGTH: 1241

TYPE: DNA

ORGANISM: Equine Influenza Virus H3N8

FEATURE:

NAME/KEY: CDS

LOCATION: (28) ..(1239)

OTHER INFORMATION:

US-10-065-133A-16

Query Match 41.1%; Score 962.6; DB 13; Length 1241;

Best Local Similarity 68.0%; Pred. No. 5.1e-268;

Matches 844; Conservative 223; Mismatches 174; Indels 0; Gaps 0;

QY 1 AGCGAAGCGAGUCUUAUUUUCUAUUGGAAAGAAUUAAGACUAACGAAUUCUGAUG 60  
 DB 1 AGCGAAGCGAGUCUUAUUUUCUAUUGGAAAGAAUUAAGACUAACGAAUUCUGAUG 60  
 QY 61 UCGAGUCUGGCAUUCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120  
 DB 61 UCGAGUCUGGCAUUCGAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 120  
 QY 121 AAGAAGUACAUUGAGGAGGACAGAGAAAGAACCCGUCACUUGAGUAGUAGUAGUAGU 180  
 DB 121 AAGAAGUACAUUGAGGAGGACAGAGAAAGAACCCGUCACUUGAGUAGUAGUAGUAGU 180  
 QY 181 GCAUUGAAUUAUUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 240  
 DB 181 GCAUUGAAUUAUUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 240  
 QY 241 GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300  
 DB 241 GAGCAAGGCGAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 300  
 QY 301 UCAACUCUGGCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360  
 DB 301 UCAACUCUGGCUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 360



QY	361	CCAAAACUUCACAAAACUUAUUUUUUGAAGACGCGAAAGCGUUAAAACUUGAAACUCUUGGC	420
Db	361	CCAAAAGTCACAAAACCTTATTTTGAAAAGATTGAAAAGATTAAAACACGGAACCTTTGGC	420
QY	421	CCUGUCUUAUUUAGAAAACAGUCUCAAUAUACCCCGAAGAGUUGACUAUAAUCCUGUCU	480
Db	421	CCCGTTCACTTTTAAAGAAATCAAGTCAAGATTAAGAACGAGAGTTGAATGTAACCCCTGGTCA	480
QY	481	GGAGACUUCAGUGCCAAAGGAGCAACGAGUAGUAUUCAGAAAGUUGUUUCCUAAACGA	540
Db	481	GCGAGCTCAGTCCCAAGAGAGCAACAGATGAGTATGAGAAAGTTGTTTCCCAATGAA	540
QY	541	GUGGGGGCCAGAGAUACUAAAGUCGAGAUUGGCAUUAUCAAUAACCAAGAGAAAAAGAA	600
Db	541	GUGGAGCCAGAAATTCATCAATCGAAATCAACAATTAACATTAACCAAGAAAAAGAA	600
QY	601	GAACTCCAGAGUUGCAAAAUUUACACCUUUAAGUUGUCUUAACUUAAGAGAGACU	660
-	601	GAACTCCAGAGACTCCAAAATTGCCCCCTTGAATGTAAGCATACATGCTTAAGAAAGAGTTG	660
QY	661	GUCCGAAAAACGAGAUUUUCUCCAGUGUGUGUGGAAACAGCAAGUGUGUACUUAAGUG	720
Db	661	GUCCGAAAAACAAAGATTCTCCCAAGTGGCTGGGCGAAACAGCAGTGTATATCATTTGAAGTG	720
QY	721	UUGCACTUUGACUCAAAGAAACUUCUGGAAACAGAUUGUACUUCACUCCAGUGGAGAAAGUAGG	780
Db	721	TTGCACTCGACTCAGGGAACATGCTGGGAAACAAATGTACACCCAGAGACAAAGTTAGA	780
QY	781	AAGUAGUAGUUGAUCAAAAGUCUAUUAUUGGACCGAGAGCAUUGUGAAAGACAGCA	840
Db	781	AACGATGACATTGATCAAGATTAAATTAATTTGCTGCCGGAACATAGTGAAGAGCGACA	840
QY	841	GUUACGACGAGUCCACUAGCAUUCUUUAUUGAGAUUGGCCACAGCAACAGAUUGCGGG	900
Db	841	GTAATCAGCAGATCCACTACATCCCTGCTGGAATATGTCACACATGACAGATTGGTGA	900
QY	901	ACAAGAUUGUGUACAUCUUAUUGGCGAAACCCAAACGAAGAGCAAGCTUUGGAAUAUUC	960
Db	901	ATTAAGAAATGTAAGACATCTTAAAGCAGAATCCAAACGAAGAAACAGCTGTGAATATATC	960
QY	961	AAGGUGGCAUUGGGAACUGAGAUCCAGCTUACUCCUACAGUUUUUGGCGGUAACUUAAG	1020
Db	961	AAAGCAGCAATGGGGTTAAGATTAGCTCATCACTTACGCTTGTGTGGAATTCAACCTTAA	1020
QY	1021	AGAACAGCGGAUVCAGUCUCAAAGAGAGAAAGAAAGUCUCUUAACGGGCAUUCUCAAACA	1080
Db	1021	AGAACAGCGGATCATCTAGCTCAAGAGAGAAAGAAAGAAATCTTAACGGGCAACCTTCAACA	1080
QY	1081	UUGAAAAUAAGGUGCAUGAGGGAUUCGAGAGAGUUCACAAUUGUUGGCAAAAAGGCAACA	1144
Db	1081	TTGAAAAATAGAGTGCATAGAGGCTATGAAAGATTCAACATAGGTTCGGAAGAAAGACACA	1144
QY	1141	GCUAUAUCUCAAAGAAACCAAGAGAUUGAUUCACUUCUUGAGUGUGGAGAGACGAA	1200
Db	1141	GCCATTCTCAGAAAGCAACCAAGAAAGATTCAATTGATAGTAAGTGGAGAGATGAA	1200
QY	1201	CAGUGCAUAGCUGAAGCAUAUAUUUGGCGCAUGGUAUUUUC	1241
Db	1201	CAATCAATTGCTGAAGCAATTAATTGTAGCCATGCTGTTTTTC	1241

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RESULT 7
US-10-065-133A-22
: Sequence 22, Application US/10065133A
: Publication No. US20030199074A1
: GENERAL INFORMATION:
: APPLICANT: Dowling, Patricia W.
: APPLICANT: Younger, Julius S.
: TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
: FILE REFERENCE: EO-1-C2-1
: CURRENT APPLICATION NUMBER: US/10/065,133A
: CURRENT FILING DATE: 2002-12-10

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? PRIOR APPLICATION NUMBER: PCT/US99/16583
? PRIOR FILING DATE: 1999-08-12
? PRIOR APPLICATION NUMBER: 09/133,921
? PRIOR FILING DATE: 1998-08-13
? NUMBER OF SEQ ID NOS: 108
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 22
?
? LENGTH: 1232
?
? TYPE: DNA
?
? ORGANISM: Equine influenza virus H3N8
US-10-065-133A-22

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Query Match	Similarity	40.2%	Score	941.4	DB	13	Length	1232	
Best Local	Similarity	44.1%	Pred.	No. 7.2e	262				
Matches	789	Conservative	261	Mismatches	181	Indels	0	Gaps	0
Qy	1111	GAGUUCACAAUUGGUGGAAAAGGGCCAAACGCUUUAUCUACGAAAAGCAACCGAGAUUG	1170						
Db	2	GAATTCACAAATGGTCGGAAAGAAAGCAACGCCATTCTCCAGAAAAGCAACCGAAGATTGG	61						
Qy	1171	AUUCAGCUGAUUUGUGAUGGAAAGCAACGACUUCGUAUACUCUAGCAAAUAUUGUGGCC	1230						
Db	62	ATTCAATTAATGTAGTAATGATGGAGAGATGAACAAATTCATTCTGAAGAAATTAATGTAGCC	121						
Qy	1231	AUGGUUUUUUACAAGAAAGAUUUGUAUUAAAAGCAUGUAGGUGAUUUGAAUUUCGAAU	1290						
Db	122	ATGGTGTGTTTCGCAAGAAAGATTGCAATGATTAAGACATTTGAGGCGAATTTGAACCTGTT	181						
Qy	1291	AUUVAGGCAAAUUCAGCGCAUUGAAUCCCAUCCAUCCAUUUUAAGCAUUUUUCAGAAAGAU	1350						
Db	182	AATAGAGCAAAATCAGAGCGCTTGAAACCCCATGCAATCACTCTTGAGGCAATTTCCAAAAGAT	241						
Qy	1351	GCGAAAGUCGCUUUUUUCAAUUGGGGAAUUGAACAUAUCCGACAUGUGAUGGCAUUGNU	1410						
Db	242	GCAAAATGCTTTTCCAGAAATTGGGGAGATTGAAACCCATGCAATGTGATGGCAATGATT	301						
Qy	1411	GCGGUUUUACCAAGCAUAGACUCCCAAGCAAGAGUUGUCAAUAGAGGGGUAUAGGUCAGC	1470						
Db	302	GGAATTAATTTGCTCGTCAATGACCCCAAGCAACGAGATGTCAATTTGACAGAGATGAGAGTCA	361						
Qy	1471	AAAUUGGGCGUGAGUAGUAUUCUCCAGCGCGGAGAGAUAGUGUGUAGACAUUGACCGGUGU	1530						
Db	362	AAAATGGGAGTGCATGAGTACTCCAGACCTGAGAGATGGTGTGAGACATTGACCGTTT	421						
Qy	1531	UUGAGAGUUCGAGACCAACGAGGAAUUGUACUAUACUCCUGAGAGGUCGUGAAACA	1590						
Db	422	TTAAGAGTCCGGATCAAAAGGAGAAACATCTACTGTCCTCGTAAGAGTCAAGTGAACAA	481						
Qy	1591	CAGGGAACACAGAAACUAGACAAUAAUCUACUACUACUACUACUACUACUACUACUACU	1650						
Db	482	CMAAGAAACGAAAGCTGACAAATTAATTTATTCATCAATCAATGATCTGGAGATTTAAATGCT	541						
Qy	1651	CCUGAGUCAGUGUGUGUCAAUCCUACUACUGUAGUACUACGAAACUUGGAAACUGUAAA	1710						
Db	542	CCGAAATCAGTGTGGTTCATACTTATCAATGATCATCAGAACTGGGAAATTTGTGAA	601						
Qy	1711	AUUCAGUGUCUCGAAUUCUUAUGCCUAUACUAUAAAUAUGAAUUUGAGCCAUUUUCAG	1770						
Db	602	ATTCAATATGTGCACAGGATCCCAAAATGTTATACAAATTAAGATTAAGATTGAGCACTTCAG	661						
Qy	1771	UCUUUAGUUCUAAAGGCCAUUAGGCCCAUAUACGUGGUGUUUGUGAGACUCUAUUCCAA	1830						
Db	662	TCCCTGTGCTCTTAAGGGCCACAGAAAGCCAAATACGCGGTTTCTGTAAAGAACCTCTGTTCCAG	721						
Qy	1831	CAAUUAGAGGAGUUAUUGGAGCAUUUGUAUCCACCAAGAAUAUAAAACUUCUUCUCCUU	1890						
Db	722	CAAAATGCGAGATGTACTTTGAAACATTTTGATCTGCTCAAAATTAATTAACCTCTCCCTTTT	781						
Qy	1891	GCACCCGCCCCCAAGAAAGAAUAGAUUGCAGUUCUUCUACGACUAGCUGUAUUGUAGG	1950						
Db	782	GCCGCTGCTCTCTCCGGAACAGAGTAAAGATGAGTCTTCTTTGACGCTTAATGTAAAG	841						
Qy	1951	GGAUCAGGAUAGCAUAUUCUUGAAGGGCAUUCUCCUAUUAUUCACUACACAGACC	2010						

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Db      842  GGAATGGGAATGAGGATCTTGTAAAGGCAATTCCTCCAGTTCACTCAATTAAGCC 901
Qy      2011  ACUAAAGACUACAUUUUCUGAAAGAGUCUGGCACTUUUAACUAAAGACCGAGUAGA 2070
Db      902  ACTAAGAGGCTGACAGTCTCTGAAAGAGATGACAGGTGCGCTTACTGAAGCCAGATGAA 961
Qy      2071  GGCACAUUCUGAGUGAGUCGCGUGUUCUGAGAGAUUCUUAUUCUGGCAAAAGAAU 2130
Db      962  GGTACGCTGGAGTAGATCTGCTGTCTAAAGAGGTTCTCAATTTAAGTAAAGAAAC 1021
Qy      2131  AGGAGAUAGACACGAGAUUAAGAUCAUAGAAACUAGUAACUUGGAAAGAGAAAG 2190
Db      1022  AAGAGATATGACCGAGCACTAAGCATATGAACTGACAACTTGCAAAAAGGAGAA 1081
Qy      2191  GCUAUAUACUAAUUGGCAAGAGACGUGUGUGUAUUAAGAAACGAAACGAAACUCU 2250
Db      1082  GCTAATGTGCTAATTTGGGCAAGGGGACGTGTGTGTAATGAACCGAAACCTGACTCT 1141
Qy      2251  AGCAUACUUAACUAGACCGCAGACGAGCAACCAAAAGAUUCGAGUGGCAUUAUAGU 2310
Db      1142  AGCATACTTACTGACAGCCAGACGAGCAACCAAAAGATCGATGCGCATATATGTGT 1201
Qy      2311  UGAUAUAGUUAUAAAAGCAACCUUGUUCUACU 2341
Db      1202  TGAATGTGTTAAAAAGCACTTGTCTACT 1232

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## RESULT 8

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US-10-065-133A-19
; Sequence 19, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OR INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(1196)
; OTHER INFORMATION:
US-10-065-133A-19

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Query Match      40.2%; Score 941.4; DB 13; Length 1233;
Best Local Similarity 64.1%; Pred. No. 7,2e-262;
Matches 789; Conservative 261; Mismatches 181; Indels 0; Gaps 0;

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Qy      1111  GAGUUCACAUAUGUGUGGAAAGAGGCAACGCUUAUCUGAGAAAGCAACGAGAGAUUG 1170
Db      3      GAATTCAATGTGTCGGAGAGAGGCAACAGCCATCTCTCAGAAAGCAACAGAAATGTC 62
Qy      1171  AUUCAGCUGAUUUGAGAGAGAGAGACAGUCGUAAGCUGUAAGCAUAUAUUGUGGCC 1230
Db      63      ATTCAATTGTATGATGAGTAGGAGAGATGAACAATCAATCTCTGAAGCAATTAATTTAGCC 122
Qy      1231  AUGGUAUUUUCACAAAGAAUUGUAUUAAGCAAGUUAAGAGUGUACUGAAUUCGU 1290
Db      123  ATGCTGTTTTCGCAAGAGAAATTCATATAAAGCAATTCGAGCGCATTTGAACTTCGT 182
Qy      1291  AAUAGGCGCAAAUUCGCAUUGAUAUCCAUUGCAUUCUUAUUAAGCAUUAUUCGAAAGAU 1350

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Db      183  AATAGAGCAATTCAGCGCTTGAACCCCATGCATCACTCTTGAAGCATTTCCAAAAGAT 242
Qy      1351  GCGAAAGUCUUUUUCAAUAUUGGGAAUUGAAUAUUGCAUAUUGCAUAUUGGAAUUGAU 1410
Db      243  GCAAAAGGCTTTTCCAGAAATTGGGAGATTGAACCATCGAACATGTGATGAGGAATGATT 302
Qy      1411  GGGGUAUUAACGACAGUACUACUCCAGACAGAGAUUGCAUAGAGGGGUAAGAUUCAGC 1470
Db      303  GGAATATTCCTCGACATGACCCCAAGCAACGAGATGTCAATTGAAGAGGTGAGATCGAC 362
Qy      1471  AAAAUGGCGUGUAUGAUAUAUCUACGCGCGGAGAGAGUAUGUGUAGCAUUGACCGGUTU 1530
Db      363  AAAATGGAGTGTGATGATGATCTCCAGCACTGAGAGAGTGTGTGATGATGATGATGATGAT 422
Qy      1531  UUGAGAGUUCGAGACCAACGAGAAAUUGUACUAUUCUCCUGAGAGAGUACUGAAACA 1590
Db      423  TTAAAGTTTCGGGATCAAAAGGGGAAACATATCTACTGTCCTCCGAAAGAGTCACTGAAACA 482
Qy      1591  CAGGGAACAGAGAAACUGACAUUAACUUAUCUACUUCGUAUUGAGUGGAGAUUAUAGCC 1650
Db      483  CAAGGAACGGAATAAGCTGCAATTAATTTATCATCATCATCATCATCATCATCATCATCAT 542
Qy      1651  CGUGAGUACUGUGUGUACUAUUCUUAUGAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1710
Db      543  CCCGATTCAGTGTGTGTGATCTTATCATATGATCATATGAGACTGAGAAATTTGAA 602
Qy      1711  AUUCAGUGUCUACAGAUUCUUAUUGCUUAUAUAUUAUUAUUAUUAUUAUUAUUAUUAU 1770
Db      603  ATTCAATGTGTCACAGAGATCCCAAAATGTTATATCAATTAATTAATTAATTAATTAATTA 662
Qy      1771  UCUUAUUGUCUUAAGCCCAUUAUAGCCCAUAUACAGUGGUGUUGUUAAGACUUAUUCGA 1830
Db      663  TCCCTGTGTCCTTGAAGGCGCAACCAAAATACACGCGTTTCTGTAAGAAACCTGTGTTGAG 722
Qy      1831  CAAUAGAGGAAUUGUACUUGGGGCAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1890
Db      723  CAAATGCGAGATGATCTTGAACCATTTATATCTGCTCAAAATTAATTAATTAATTAATTA 782
Qy      1891  GCAGCGCGCCCAACCAAGAAAGAAUUAUUGAGUUCUUCUUAUUAUUAUUAUUAUUAUUAU 1950
Db      783  GCGCGTGTCTCCCGGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 842
Qy      1951  GGAUACAGAGAUAGAAUUAUUGUUAAGGCGCAAUUUCUUAUUAUUAUUAUUAUUAUUAU 2010
Db      843  GGATCGGAATGAGATCTTGTAAAGAGCAATTCCTCAGTGTCAACTAACATTAAGCC 902
Qy      2011  ACUAAAGACUACUAUUCUUGGAAAGAUUCUGGCACTUUUAACUAGAACCCAGAUAGA 2070
Db      903  ACTAAGAGGCTTCACAGTCTCTCGAAAGATGCAAGTGCCTTAATGAAAGACCCAGATGAA 962
Qy      2071  GGCACAUUCUGAGUGAGUGCGUGUGUUGAGAGAUUCUUAUUCUGGCGCAAAAGAAU 2130
Db      963  GGTACGCGCTGAGATGAAATCTCTGTCTTAAGAGGTTTCTCATTTTAAAGTAAAGAAAC 1022
Qy      2131  AGGAGAUUUGACCGACGACUUAAGCAUUAUGAAACUGAGUAAACUUGGCAAAAGAGAAAG 2190
Db      1023  AAGAGATATGCGCCAGCACTAAGCATCAATGAATGAGCAAAACCTTGCAAAAGGGAGAAA 1082
Qy      2191  GCUAUAUUAUUAUUGGCGCAGAGAGAGUGUGUGUUAUUAAGAAACGAAACGAAACUCU 2250
Db      1083  GCTAATGTGCTAATTTGGGCAAGGGGACGTGTGTGTAATGAAGAAACGTAACCTCT 1142
Qy      2251  AGCAUACUUAUCGAGACGACGACGACGACCAAAAGAUUUGGAGGCAUUAUUAUUG 2310
Db      1143  AGCATATCTTACTGACAGGCAAGACGACGACCAAAAGATTCGATGCGCATCAATTAATGTGT 1202
Qy      2311  UGAUAUAGUUAUAAAAGCAACCUUGUUCUACU 2341
Db      1203  TGAATGTGTTAAAAAGCACTTGTCTACT 1233

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## RESULT 9

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US-10-065-133A-15
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; Sequence 15, Application US/10065133A
; Publication No. US2003019074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; '0-065-133A-15

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Query Match 40.1%; Score 940.4; DB 13; Length 1214;
Best Local Similarity 68.0%; Pred. No. 1.4e-261;
Matches 825; Conservative 218; Mismatches 171; Indels 0; Gaps 0;

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QY 28 AUGGAAAGAAUAAAGAACTUACGAAUUCGAGUUGCGACUCGCGGAGAUACUA 87
DB 1 ATGGAGAAATATTAAGAACTGAGAGATCTAATGTCAATCCCGGAGAGATACTA 60
QY 88 ACAAATAACACAGUGACCAUUGGCGCAUUAUUAAGAAUUAACUACUAGGAGGAGAA 147
DB 61 ACAAATACTACTGTGACCACTGGCCATATCAATCAAGAAATACACACTCAAGAAAGAG 120
QY 148 AAGAACCCGUCACUAGAGUAGAAUUGAGUAGGCAUAGAAUUAUCCGAAUUAAGCCGAC 207
DB 121 AAGAACCCGCACTTAGAGTGAAGTGAATGATGAGAAATGAATCAAGGAGGAGAT 180
QY 208 AAGAGAAUUAACGAAUAGUUAUUCUGAGAGAAUUGAGCAAGGCGAAACUUAUUGAGUAA 267
DB 181 AAGAGATATATGAAATGATCTCTGAGAGAAATGAACAGGCGCAAAACCTTTGGAGCA 240
QY 268 AUGAGUAGUUGCCGAGUUGGAGUUGUUAUACUUCUGGCGUAGUACUUGUGAGAU 327
DB 241 ACGAAGATGCTGCTGACAGACCGCTAATGTATCATCTGCGACATGATGTGAGAT 300
QY 328 AGAAUUGACCAUUAAGAAUUGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 387
DB 301 AGGAATGACCAACAGACGACATCTTATTCGAAAGCTACAAATCTTATTTGAA 360
QY 368 AAAAGCGAAAGGUAUAAACUUGAAACUUAUUGCCCGUUAUUAUUAUUAUUAUUAUUA 447
DB 361 AAAAGTTGAAGTTAAACAGGAACTTTGGCCCCGTTCAATTTAGAAATCAAGTCAAG 420
QY 448 AUAAGCCGAAAGUUGACUUAUUAUUCUGUACUAGACUUCAGUGGCCAAGAGGACAG 507
DB 421 ATTAACGAGAGGTTGATGTAAACCTGCTACGCGGACCTCAGTGCAGCAAGAGACAA 480
QY 508 GAUGUAUUAUGAUGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 567
DB 481 GATGTGATCATGAAAGTTGTTTCCCAATGAAAGTGAAGGAGCCAGAAATCTTACATCGAA 540
QY 568 UCGCAUUAUUAACAAUUAACAAAGAGAAUUAAGAAAGAAUUAUUAUUAUUAUUAUUAUUA 627
DB 541 TCACAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 600
QY 628 UUGAGUUGUUGCUAUAUUGUUAAGAGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 687
DB 601 TTGATGTGATCATGATCTAGAAAGAGGTTGTGTCGAAUUAUUAUUAUUAUUAUUAUUAUUA 660
QY 688 GCUUGUGAAACAAAGAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 747
DB 661 GCTGCGGAGAAACAGAGTGTATATCAATTGAAGTGTTCATCTGACACAGGAAACATGCTCG 720

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QY 748 GAACAGAUUACATTCAGAGUAGAAUAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 807
DB 721 GAACAAATGTACCCCGAGAGAGAAAGTTAGAAAGAAAGATGATCAAAAGTTTAATTT 780
QY 808 AUGGACCCGAGAGUAGUAGAAAGAGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 867
DB 781 ATTCTGCTCCGAAACATATGTAAGAAAGAGACATGATCAAGAGATCTACATGATCCCTG 840
QY 868 UUGAGAUUGGCCAGACACAGAUUUGCGGACAGAGUUGGAGUAGUUAUUAUUAUUAUUAUUA 927
DB 841 CTGAAATGTCACAGTACAGATTTGATGAATTAAGATGGTGAACATCTTAAAGACAG 900
QY 928 AACCCAAAGAAAGAGACAGUUGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 987
DB 901 AATCCAAACAGAGAAACAGCTGTGATATATCCAAAGCAGCAATGAGTTAAAGATTAAC 960
QY 988 UCAUCCUAGUUGGCGGAGUACAUUUAUUAAGAAACAGGAGUACUAGUACAGAGA 1047
DB 961 TCATCATTTACGCTTTGTGATTTACCTTTAAGAGAAACAGTGTATCATCTACAGAGAGA 1020
QY 1048 GAGAAAGAGUUGUUAAGGCAUUCUUAACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1107
DB 1021 GAGAAAGAAATGCTTACGCGCAACCTTCAAACTTGAATTAAGATGATGAAGGCTAT 1080
QY 1108 GAGAGUUAUUAUUGGAGAAAGGCGCAACAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1167
DB 1081 GAAGAAATTCACATATGTGTGAGAAAGAGAGCAACGCAATCTCAGAAAGGCAACAGAA 1140
QY 1168 UUGAUUACAGUUGUUGAGUAGAGAGAGAAACAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 1227
DB 1141 TTGATTTCAATGATATGATTAAGTGTGAGAGATGAACATCAATTCGTAACCAATTAATGTA 1200
QY 1228 GCCAUGGUAUUAUUC 1241
DB 1201 GCCATGCTGTTTC 1214

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RESULT 10
US-10-065-133A-18
; Sequence 18, Application US/10065133A
; Publication No. US2003019074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1214
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; US-10-065-133A-18

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Query Match 40.1%; Score 938.8; DB 13; Length 1214;
Best Local Similarity 68.0%; Pred. No. 4.1e-261;
Matches 825; Conservative 217; Mismatches 172; Indels 0; Gaps 0;

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QY 28 AUGGAAAGAAUAAAGAACTUACGAAUUCGAGUUGCGACUCGCGGAGAUACUA 87
DB 1 ATGGAGAAATATTAAGAACTGAGAGATCTAATGTCAATCCCGGAGAGATACTA 60
QY 88 ACAAATAACACAGUGACCAUUAUUGGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 147
DB 61 ACAAATACTACTGTGACCACTGGCCATATCAAGAAATACACATCTCAGAAAGAGAG 120
QY 148 AAGAACCCGUCACUUAUUGAGUAGAAUUGAGUAGGCAUUAUUAUUAUUAUUAUUAUUA 207

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Db      121  AAGAACCCCGCACTTGTAGATGAAGTGAATGACATGAATACCAATTAACAGAGAT 180
Qy      208  AAGAGAGAUAAAGAAAUGAUUUCUGAGAGAAUAGACAAAGGCAAAUCUUAUGAGAUAA 267
Db      181  AAGAGATTAATGAAAATGATTCCTGAGAGAAATGAAACAGGGGAAACCTTTGGAGCAA 240
Qy      268  AUAUGAGAUUCCCGAUGCGAUGCGUGAUGUAUACCCUUGCGUGAUGAUGAUGAUAU 327
Db      241  ACCAAGATGCTGGCTCAGACCCGTAATGTATCACTCTGCAATGTCATGTGTGAAT 300
Qy      328  AGAAUUGACCAUUGACAAGUACGUUACUUAUUGCAAAAAUUAACAUAUUUUGAG 387
Db      301  AGGATATGACCAACAAAGACCAATTCATTAATCAAAAGTCAAAAATTATTTTGA 360
Qy      388  AAAAGUGAAAGUUUAAAACUAGAACCUUUGGCCUUGUCCAUUUUAGAAACCAAGUCAA 447
Db      361  AAGATTGAAAGATTAAACACGGAACCTTTGGCCCGTTCAATTTAGAAATCAAGTCAAG 420
Qy      448  AUAACCCGGAAGAGUUGACAUAUAAUCCUGUACAUGACCTUCAGUCCCAAGAGCAG 507
Db      421  ATTAAGACGGAAGATTGATGTAACCTCGTCAACGCGACCTCAGTGCACAAAGACACA 480
Qy      508  GAUGUAUUGAUGGGAAGUUGUUUCCUAACGAAGUGGGGCGAGAUUUAAGUUGAA 567
Db      481  GATGTATATGAGAGTGTATTTCCCAATTAAGAGGAGCAAGATTTCAATTCGAA 540
Qy      568  UGCACAUAUUAACAUAUAAACCAAGAGAAAAGAAAGAACUCCAGAGAUUGCAAAUUCACCU 627
Db      541  TCACAATTAACAATAACCAAGAGAAAAGAAAGAACTTCAGAGCTGCAAAATTCGCC 600
Qy      628  UUGAUGUUGCGUAUUGUUAAGAGAGAAACUUGUCCGAAAAAGAGAUUUUCCGAGU 687
Db      601  TTGATGTGTAGCATACATGTCTAGAAAGAGATTGTCCGAAAAAGAAATCTCTCCAG 660
Qy      688  GUGUGUGAACAAGACGUGUGUAUUGUAUGUGUUGACUUAACUACAGAAACAGUCUG 747
Db      661  GCTGCGGGAACAAGAGTGTATATCATTTGAAGTGTTCATCTGACCTCAGGAAACATGCTG 720
Qy      748  GAACAGAUUACACUCCAGUGGAGAGAAUGAGAAUUGAUUGUUAUUAAGUUAU 807
Db      721  GAACAATTTACACCCCGAGAGAGAAAGTTAAGAAAGATGACATTTGATCAAAAGTTAAT 780
Qy      808  AUAUGACCCAGAGACUAUAGUAGAAAGAGACAGAUUACAGAUUCCAUAUUCUUA 867
Db      781  ATTGCTGCCCCGGAACATAGTAGAAGAGCGACATATCAGACATCCATGCAATCCCTG 840
Qy      868  UUGAGAUUGUCCACAGACACAGAUUGGCGGGAACAAGAUUGUGAUAUUCUUAAGCAG 927
Db      841  CTGGAATGTGCAACAGTACAGAGATGTGTGAATTAAGATGTGATCATCTTAAGCAG 900
Qy      928  AACCCAAACGAAGAGACGUGUGAAAUUAGCAAGCGUACAUUGGGAUCUGAGAUCCG 987
Db      901  AATCCAAACGAAGAACAGCTGTGATATATCAAAAGACAGCATGGGTTAAAGATTAGC 960
Qy      988  UCAUUCUUAUGUUGCGCGGUAUUCAUUUAAGAGAAACAGCGAUCAUUGAUGAAGA 1047
Db      961  TCATCATTCAGCTTTGTGATTTCACTTTAAGAAACAAAGTCAATCATCAAGTCAAGA 1020
Qy      1048  GAGGAAGAAAGUGCUUAACGGGCAUUCUUAACAUAUUGAAUUAAGGUGUACUAGAGAUAC 1107
Db      1021  GAAAGAAAGAAATCTTAACGGGCAACCTTCAAACTTGAATAATTAAGTCAATTAAGGCTAT 1080
Qy      1108  GAGGAGUUCACAUAUGUUGGAAAGGCAACAGCUUAUUCUAGAAAGCAACAGAGGA 1167
Db      1081  GAGGAATTCACAAATGCTCGAAAGAGAGACAGCAATTCCTCAGAAAGCAACCAAGGA 1140
Qy      1168  UUGAUGUACUGUUAUGUAGAGAGAGAGAAAGUAGUAGUAGUAGUAGUAGUAGUAG 1227
Db      1141  TTGATTCATTCATATGTAAGTGGAGAGATGAACAAATCAATTCCTGGAAGCAATTAATGTA 1200
Qy      1228  GCCAUGUAUUAUUC 1241

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Db      1201  GCCATGTGTTTTC 1214

RESULT 11
US-10-065-133A-23
; Sequence 23, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1195)
; OTHER INFORMATION:
US-10-065-133A-23

Query Match      40.1%; Score 938.2; DB 13; Length 1232;
Best Local Similarity 63.9%; Pred. No. 6,1e-261;
Matches 787; Conservative 261; Mismatches 183; Indels 0; Gaps 0;

Qy      1111  GAGUUCACAUUGUGGGAAGGGAACGACUUAUUCUAGAAAGCAACAGAGAUUG 1170
Db      2      GAATTCACAAATGCTGGAGAAAGCAAGCAACCAATTCGAAAGCAACAGAAAGATTG 61
Qy      1171  AUAUGCUGAUUUGUGAGUAGAGAGACGACAGUUGUACUAGCAUAUUAUUGUGGCC 1230
Db      62  ATTCAATTGATAGTAAGTGGAGAGATGAACAAATCAATTCCTGAGCAATTAATTTGAGCC 121
Qy      1231  AUGGUAUUUUCACAAGAAAGUUGUUAUUAAGCAGUUAAGCUGUAUUCGUAUUUUGGU 1290
Db      122  ATGGTGTTCGCAAGAAAGATTGCATGATACAAAGCAGTTGAGGCGGATTTGAACCTTGCT 181
Qy      1291  AAUUGGCAAAUUCAGCAUUAUUAUCCCAUCCAUCAACUUAUUAAGACAUUUUUCAGAGAGAU 1350
Db      182  AATTGAGCAAAATCAGCCCTTGAACCCCATGCACTCACTCTTGAAGGCATTTCGAAAAAGAT 241
Qy      1351  GCGAAAGUGCUUUUUCAAAAUUGGGGAUUGAAUAUUGCAUAUUGGUAUGGUAUGAU 1410
Db      242  GCAAATAGCTTTTTCAGAAATGGGGATTTGAACCCATGCAATGATGAGGAAATGATT 301
Qy      1411  GGGGUUAUUAACAGACAUAGACUCCACAGACAGAGAUUGCAUAGAGGGGUUAAGAUCCAGC 1470
Db      302  GGAATATTGCTGCTGACATGACCCCAAGACCGAAGATGTCATTTGAGAGAGTGAAGTCAAGC 361
Qy      1471  AAAAUGGGCUUAUUAUUAUCCAGCGCGGAGAGAGUAGUUGGUGAGCAUUGACCGGUUU 1530
Db      362  AAAATGGAGATGATGATGCTCCACACACTGAAAGAGTGTGTGAGCATTTGACCGTTT 421
Qy      1531  UUGGAGUUGCAGACCAAGAGAGAAUUGUAUUAUUCUUAUUCUUGAGGAGGUAAGAAACA 1590
Db      422  TTAAGATTTGGGATTCAAAGGGAAACATTAATCTGTCCTTAAGAGCTGACAGTGAACA 481
Qy      1591  CAGGAAACAGAGAAACUGACAUUAUUAUCUACUUCGUAUGUAUGUUGGAGUAUUAUGGC 1650
Db      482  CAAGAAACGGAAGAGTGAACAAATTAATTAATCAATCAATTAATGATGTGGAGATTAAATGCT 541
Qy      1651  CCUGAGUCAGUUGUGUUAUUAUCCUUAUUGAGUAGUUAUUGCAAAACUUGGAAACUUGUAAA 1710
Db      542  CCGAATCAGTGTGTGTCATTAATCAATGATCATCAGAACTGGGAAATTTGTGAA 601

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Qy	1711	AUUGAGUGUGUCUGAGAAUCUACAUGGUAACAUAUAAUAGAAUUBUGAGCCAUUUCAG	1770
Db	602	ATTCAATGATGTCACAGATATCCCAATGTTATACATTAAGATAGAAATTTGAGCCATTCCAG	661
Qy	1771	UCUUUAGUUCCUAAAGGCCAUUAGAGGCCAAUACAGUGGGUUUUUGAGACUUAUUCCAA	1830
Db	662	TCCCTGTCCTCCCTAAGGCCACCAAGAAAGCCAAATACAGCGGTTTCGTAAAGAACCTGTCTTACG	721
Qy	1831	CAAUUAGAGGAGUUAUUCUUGGACAUUUUGAUCACCCGAGUAUAUAAACUUCUUCUCCUU	1890
Db	722	CAAAATGCGAGATGTACTTGGAACAATTTATATCTGCTCAAAATPAATAAACTCTCCCTTTT	781
Qy	1891	GCAGCCGCCCCCAACAAAGCAUAGUAGAUUGCAUUCUUCUACAGUCUAGUAGUAGAG	1950
Db	782	GCCTGCTGCTCTCCCGGAACAGATAGATGCGATCTCTTCTTTGACGTTTAATGTAAGA	841
Qy	1951	GGAUACGGAUUGAGUAUACUUUGUAAAGGGCAAUUUCUUAUUCUACAUCUACAAGACC	2010
Db	842	GGATTCGGGAATGAGAGATCTTGTAAGAGGCAATTCGCCAGTGTTCAATCAATPAAGCC	901
Qy	2011	ACUAAAGAGACUAAACAUAUUCUGGAAAGAUUCUGGCAUUAUACUAAAGACCAGAUAGA	2070
Db	902	ACTAAGAGAGCTCACAGTCTCTCGGAAAAGATGACAGGTGCGCTTACTGAAGACCAGATGAA	961
Qy	2071	GGCAACUUGGAGUGGAGUCCGCGUUGUCUAGAGAGAUUCUUAUUCUGGGCAAAAGAGAU	2130
Db	962	GGTACCGCTGAGATGATGATCTGCTGTTCTTAAGAGGGTTTCTCATTTTAAGTAAGAAAC	1021
Qy	2131	AGGAGUAUUGGACCGACAUUAAAGCAUACAUGAACUAGUAACUUUGCAAAAGAGAAAAG	2190
Db	1022	AAGGATATATGCGCCCGACACTAAAGCATCAATGAACTGACAAACCTTGCAAAAGGGAGAAA	1081
Qy	2191	GCUAUAGUACUAUUGGGCAAGAGACGUGGUGUGUAGUAUAGAAACGAAACCGAACUCU	2250
Db	1082	GCTAATGCTGCTAATTTGGGAGAGGGGACGTTGGTTGTAATGAAACGAAACGTGACTCT	1141
Qy	2251	AGCAUACUUAUCUAGCAGCCAGACAGACGACCAAAAGAUUCGAGUAGCCAUACAUAUAGU	2310
Db	1142	AGCATACTTACTGACAGCCAGACAGACGACCAAAAGATTCGATGGCCATCAATTAAGT	1201
Qy	2311	UGAAUAGUUAUAAACGACACUUGUUUUAUACU	2341
Db	1202	TGAATTTGTTAAAAACGACCTTGTCTTACT	1232
RESULT 12			
US-10-065-133A-21			
pence 21, Application US/10065133A			
-dlication No. US20030199074A1			
GENERAL INFORMATION:			
APPLICANT: Youngner, Patricia W.			
APPLICANT: Dowling, Julius S.			
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES			
FILE REFERENCE: EQ-1-C2-1			
CURRENT APPLICATION NUMBER: US/10/065,133A			
CURRENT FILING DATE: 2002-12-10			
PRIOR APPLICATION NUMBER: PCT/US99/18583			
PRIOR FILING DATE: 1999-08-12			
PRIOR APPLICATION NUMBER: 09/133,921			
NUMBER OF SEQ ID NOS: 108			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 21			
LENGTH: 1194			
TYPE: DNA			
ORGANISM: Equine influenza virus H3N8			
US-10-065-133A-21			

Query Match	38.8%;	Score 907.6;	DB 13;	Length 1194;
Best Local Similarity	64.4%;	Pred. No. 4.5e-252;		
Matches 769;	Conservative 246;	Mismatches 179;	Indels 0;	Gaps 0

QY	1111	GAGUUCACAAUUGUUGGGAAAAGGGGACAGGCUUAUCUGAGAAAACCAACGAGGAAUUG	1170
Db	1	GAATTCACAATGGGTCCGAGAGAAAGACAACGCCATTCTCAGAAAGGCAACGAGAATTTG	60
QY	1171	AUUGACGUCGUAUUGUGAGUGGAGAGACGAACAGUCGCAUUGGUCGAGCAAUUATUGGCC	1230
Db	61	ATTCAATTTGATACCTTAAGTGGGAGAGATGAATCAATCAATTGCTGAAACCAATTAATTGATGCC	120
QY	1231	AUGGUUUAUUUACAGAGAAUUGUAUUGAUAUAAAGCAGUUGAGGUGAGGUAUUCUUAUUTUCU	1290
Db	121	ATGATGTTTTCGGAAAGAGATTTGCATGAATAAAGCAGTTTCGAGGCCAATTTTGAACCTTCGTT	180
QY	1291	AUAUGGGCAAUUACAGGAGUUGAUAUUGCCAGGACCAACUUAUUGAAGAAUUTUUGAAGAAU	1350
Db	181	AATTGAGCAAAATACAGCCCTTGAAACCCCATGACATCACTCTTGAGGCATTTTCCAAAAGAT	240
QY	1351	GCGAAAGUGUCUUAUUCAAAUAUUGGGGAAUUGAACAUAUCCAGCAUAUUGGAAUUGGAAU	1410
Db	241	GCAAAAGTCCTTTTCCAGAATTTGGGGGATTTGAATCCATCGACAAATGATGATGGGAAATGATT	300
QY	1411	GGGGUUAUUCACAGCAUUGACUCCAGACACAGAGAUUGCAUUGAGAGGGGUAAAGUACAC	1470
Db	301	GGAATATTGCTGACATGACCCCAACACCCAGATGATCATTTGAGAGAGAGTGAAGTCAAGC	360
QY	1471	AAAUAUGGCGCUAUAUUAUAUUCACGCGGAGAGAGUUGUGUGUGAAUUGACCGGUAU	1530
Db	361	AAAATGGGAATGTGATGTGATCTCCAGACATGAAAGATGGTGTGTGACATTTGACCCGTTT	420
QY	1531	UUGAGUUGUGAGACCAACAGAGAAAUGUUCUAUCUAUCUCUGAGAGGUCACUGAAACA	1590
Db	421	TTAAGATTTGGGATTCAAAGGGAAACATATCTACTGTCCTTGAAGAGTCACTGTAAGACA	480
QY	1591	CAGGGAAACAGAGAAACUGACAAUUAUCUACUCUACUUGCAUUGAGUGGCGAAUUAUUGCC	1650
Db	481	CAAGCAACGAAAAAGCTGACAAATTAATTATTCATCATCAATGATGTGGGAGATTTAAATGCT	540
QY	1651	CCUGAGUACAUUGUUGUICAUUACCUUUAUGUUAUUGAAUUCUGGAAAACUGUUA	1710
Db	541	CCCCAATTCAGTGGTGGTCTCAATCTTATCAATGGATCTACAGAACTGGAAAATTTGTAA	600
QY	1711	AUUGAGUGGUCUCGCAUUGCCUACAUUGCUUAUUGAAUUGGAAUUTUGAGCCAUUUCAG	1770
Db	601	ATTCAATGTGTACACAGATTCACACCATTTTATACATTAAGATTAAGATTGAGCCATTCACAG	660
QY	1771	UCUUAUUGUCUUAAGGCCAUUAGAGGCCAAUACAGUGGUGUUTUUGAGACUCUAUUCCAA	1830
Db	661	TCCTGTGTCCTTAGGGCCACAGAAAGCCAAATACAGCGGTTTTCGTAAGAAACCTGTTTCAG	720
QY	1831	CAAUUGAGGAGUUAUCUUGGACAUUUGAUAUCCACCCAGAAUUAUAAACUUCUUCUCCU	1890
Db	721	CAAAATGTGAGATGTACTTTGGAAACATTTGATTACTGCTCAAAATTAUAAACCTCTCTCTTTT	780
QY	1891	GCACCGCCGCCACAAAGCAAAAGUAGAAUUGCAGUUCUUCUACACUGACUGUAGUUGAGG	1950
Db	781	GCCCTGTCTCTCCGGAACAGATGAGATGACAGTTCTCTTCTTTGACTGTTAATGTAAGA	840
QY	1951	GGAUCACAGAAUUGAGAAUUAUCUGUAAAGGGGCAUUCUCCUUAUUAUCAAACACACAGACC	2010
Db	841	GGATTCGGGAATGAGAGATTACTTTGTAAGAGGCAATTCGCCAGTGTTCACACTAATAAAGCC	900
QY	2011	ACUAAAGAGACUAACAUUUCUGGCAAGAGUUGCUGGCACUCUUAUCUGAAAGCCCGAGUAGA	2070
Db	901	ACTAAGAGAGCTCAACAGTCTCTGGAAAGAAATGCAAGTCCGCTTACTGAAAGACCCAGATGA	960
QY	2071	GGCACAUCUGGAGUGAGUUGCCGUGUUCUGAGAGAUUUCUCCAUUUCUGGCGCAAAAGAGAU	2130
Db	961	GGTACCGCTGAGTAGTAATTCGTCTGTTTAAGAGGCTTTCTCATTTTAAGTAAAGAAAC	1020
QY	2131	AGGAGAUUUGACACAGCAUUAAGCAUUCAAUUGAAACUGAGUUAACUUGCGAAAGAGAAAG	2190
Db	1021	AAGAGATATGGCCACAGCACTAAGCATTAATGAATCTGAGCAAAATTTGCAAAAGGGAGAA	1080
QY	2191	GCUAUUGUACUAUUGGGACAGAGACGUGGUGUUGUAUUGAAACGAAACCGAACUCU	2250

Accession	Sequence	Length
Db	1021 AAGAGATTGGCCCGACGACTTAAGCATCAATTAACGTGAGCAAACTTGGCAAAAGGGGACAAA	10880
QY	2191 GCUAUAGACUAUATUGGGCAAGAGACGUGUGUUGUAUAGAAACGAAACGAAACUCU	2250

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Db 1081 GCTAATGCTGTAATTTGGGCAAGGGGACGTGCTTGTGTAAATGAAACGAAAGCTGACTCT 1140
Qy 2251 AGCAUACUUAUCUGACAGCCAGACGACGACCAAAAGAGUUCGAGCCAUCAU 2304
Db 1141 AGCATCTTACTGACAGCAGACGACGACCAAAAGAGATTGGATGCGCATCAAT 1194

RESULT 13
US-10-065-133A-25
; Sequence 25, Application US/10065133A
; Publication No. US2003019074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; RIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-25

Query Match 38.6%; Score 904.4; DB 13; Length 1194;
Best Local Similarity 64.2%; Pred. No. 3.8e-25;
Matches 767; Conservative 246; Mismatches 181; Indels 0; Gaps 0;

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Qy 1171 AUUCACUGUAGUUGAGUGAGAGAGACGAAAGUGUAGUAGUAGUAGUAGUAGU 1230
Db 61 ATTCAATTGATGTAAGTGGAGAGATGAGCAATCAATTGCTGAAGCAATATTGTACC 120
Qy 1231 AUGCUAATUUCACAGAAAGAUUGUAGUAAAGCAAGUAGUGAGUAGUAGUAGU 1290
Db 121 ATGGTGTTCCTCCAGAGAGATTGATGATACAGAGATTCCAGAGATTGAACCTGTT 180
Qy 1291 AAUAGGGCAANUCAGAGUUGAUAUCCCAUUGCAUUCUUAAGACATUUAACAGAU 1350
Db 181 AATTAGAGCAAAATCAGCGCTTGAAACCCCATGATCACTCTTGAGGCAATTTCCAAAAGAT 240
Qy 1351 GCGAAAGUGUCUUAUUAUUGGGGAAUUGAACAUAUUCGACAAUUGAGUGAGAAU 1410
Db 241 GCAAAAGTGCTTTTCAGAGATTGGGGGATGTAACCATCGACATGTATGGGAATGATT 300
Qy 1411 GGGGUUAUACAGACAGUACUCCAAAGCAACAGAGUAGUAGUAGUAGUAGUAGU 1470
Db 301 GGAATATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy 1471 AAAAAGGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1530
Db 361 AAAATGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 1531 UUGAGAGUUGAGACCAAGAGAAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1590
Db 421 TTAAGAGTTTCGGGATCAAAAGGAGAAACATATCTGCTCCCTGAAGAGTCAAGTAAACA 480
Qy 1591 CAGGAGACAGAGAAACUGAACAAUUAUCUAGUAGUAGUAGUAGUAGUAGUAGUAG 1650
Db 481 CAAGACAGAGAAACCTGACATATATTTATTCATCATCAATGATGATGATGATGATGAT 540
Qy 1651 CCUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1710
Db 1710
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Db 541 CCCGATCAGTGTGTCATATCTTATCATGATGATCATGAGAACTGGAATTTGAAA 600
Qy 1711 AUUCAGUGUUCUAGAAUCCUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1770
Db 601 ATTCAATGCTGACAGAGATCCCAAGATTTATCAATTAAGATTAAGATTTAGGACATTCAG 660
Qy 1771 UCUIUAGUUCUAAAGGCAUUAAGGCGCAUUAACAGUGUGUUGUUGAGACUUAUCCAA 1830
Db 661 TTCCTGTCTCTAGGGCACAGAAAGCAATACAGCGCTTCTGTAAGAACCTGTCTTTCAG 720
Qy 1831 CAUUAAGAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1890
Db 721 CAATTCGAGATGATCTTCTGAAACATTTATCTGCTCAATTAATTAATTAATCTCTCTTTT 780
Qy 1891 GCAGCGCGCCCAACCAAGAGAAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1950
Db 781 GCGGCTCTCTCTCGGAAACAGAGATGAGATGACAGTCTCTCTTGTGATGTTAATGTAAGA 840
Qy 1951 GGAUACAGAAUAGAAUUAUCUUGAAGGCGCAUUAUUCUUAUUAUUAUUAUUAUUA 2010
Db 841 GGATCGGAAATGAGATATCTGTAAGAGCAATTTCCCACTGTTCAACTCAATTAAGGCC 900
Qy 2011 ACUAAAGACUAAACAAUUCUGGAAAGAGAGAGUAGUAGUAGUAGUAGUAGUAGUAG 2070
Db 901 ACTAAGAGCTCAAGCTCTCGAAGAAAGATGACAGTGGCTTACTGTAAGACCCAGATGAA 960
Qy 2071 GGCACAUUCUGAGUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 2130
Db 961 GGTACGCGCTGAGAGATGAGATGCTGTTCTTAAGAGGGTCTTCAATTTAGTAAAGAAAC 1020
Qy 2131 AGGAGAAUAGAGACCAAGCAUUAUUAAGCAUUAUUAUUAUUAUUAUUAUUAUUA 2190
Db 1021 AAGGAAATATGCGCCAGCACTAAGCATCAATGAAGTGAAGCAATTTGCAAAAGGAGAAA 1080
Qy 2191 GCUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2250
Db 1081 GCTAATGCTGTAATTTGGGCAAGGGGACGTGCTGTGTATGTAAGAGAAAGCTGACTCT 1140
Qy 2251 AGCAUACUUAUCUGACAGCCAGACGACGACCAAAAGAGUUCGAGUAGUAGU 2304
Db 1141 AGCATCTTACTGACAGCAGCAGACGACGACCAAAAGAGATTGGATGCGCATCAAT 1194

RESULT 14
US-09-971-372A-15/c
; Sequence 15, Application US/09971372A
; Publication No. US20030035814A1
; GENERAL INFORMATION:
; APPLICANT: Kawaoka, Yoshihiro
; APPLICANT: Neumann, Gabriele
; TITLE OF INVENTION: Recombinant Influenza viruses for vaccines and gene
; FILE REFERENCE: 960296, 98130
; CURRENT APPLICATION NUMBER: US/09/971, 372A
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: PCT/US00/09021
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/127,912
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(12)
; OTHER INFORMATION: BsmBI recognition sequence
; FEATURE:
; NAME/KEY: misc feature
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# OM nucleic - nucleic search, using sw model

Run on: December 31, 2003, 16:20:25 ; Search time 4425 Seconds  
(without alignments)  
12858.029 Million cell updates/sec

Title: US-08-573-569-15

Perfect score: 2341 1 AGCAGAGACGACGCAUUAU.....AAAACGACUUCUACU 2341

Sequence: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues 45562784

1 number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estopl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C 1	56.4	2.4	997	29	CNS005TE	AL060767	Drosophila
C 2	50	2.1	1201	13	BX381961	BX381961	BX381961
C 3	49.4	2.1	1089	9	AL525517	AL525517	AL525517
C 4	48	2.1	1101	29	CNS017KC	AL108171	Drosophila

Result	No.	Score	Query Match	Length	DB	ID	Description
C 5	46	2.0	1089	13	BX351150	BX351150	BX351150
C 6	45.8	2.0	1101	29	CNS0182P	AL108811	Drosophila
C 7	45.4	1.9	1101	29	CNS0039G	AL063921	Drosophila
C 8	45	1.9	1201	13	BX361080	BX361080	BX361080
C 9	44.6	1.9	1101	29	CNS0006J	AL062049	Drosophila
C 10	43.8	1.9	833	13	BUT71589	BUT71589	BUT71589
C 11	43.8	1.9	1204	29	CNS016E2	AL106628	Drosophila
C 12	43.6	1.9	1000	29	CNS0061A	AL061657	Drosophila
C 13	43.4	1.9	204	28	AZ045148	AZ045148	Gm Umb001
C 14	43.4	1.9	1201	13	BX376097	BX376097	BX376097
C 15	43.2	1.8	1202	29	CC300546	CC300546	CC300546
C 16	42.8	1.8	1202	29	CC300546	CC300546	CC300546
C 17	42.6	1.8	1201	9	AL564647	AL564647	AL564647
C 18	42.2	1.8	537	13	BUT498263	BUT498263	BUT498263
C 19	42.2	1.8	1054	13	BX432381	BX432381	BX432381
C 20	42.2	1.8	1101	29	CNS0106X	AL098595	Drosophila
C 21	42	1.8	1101	29	BM160400	BM160400	BM160400
C 22	42	1.8	1101	29	CNS00E7Y	AL069057	Drosophila
C 23	42	1.8	1101	29	CNS0181N	AL108773	Drosophila
C 24	42	1.8	1101	29	AL697277	AL697277	AL697277
C 25	41.8	1.8	1842	9	AL661310	AL661310	AL661310
C 26	41.8	1.8	1021	13	CNS00133	AL074369	Drosophila
C 27	41.4	1.8	1178	13	BX397483	BX397483	BX397483
C 28	41.2	1.8	415	28	B51092	B51092	B51092
C 29	41.2	1.8	928	29	CNS0102F	AL108415	Drosophila
C 30	41	1.8	928	29	CNS0102F	AL108415	Drosophila
C 31	41	1.8	1630	12	BM807552	BM807552	BM807552
C 32	40.2	1.7	938	29	CNS006TJ	AL065906	Drosophila
C 33	40	1.7	871	28	AZ545448	AZ545448	ENTD181TR
C 34	40	1.7	987	29	CNS00418	AL066537	Drosophila
C 35	39.8	1.7	308	10	BB286390	BB286390	BB286390
C 36	39.6	1.7	667	28	AQ576071	AQ576071	nbx00088F
C 37	39.6	1.7	439	28	AQ571562	AQ571562	HS 5370 B
C 38	39.6	1.7	994	13	BX414650	BX414650	BX414650
C 39	39.4	1.7	570	9	AL442893	AL442893	AL442893
C 40	39.4	1.7	620	14	CA036638	CA036638	ssalob004
C 41	39.4	1.7	707	29	AG013811	AG013811	Homo sap1
C 42	39.4	1.7	1025	13	BX387097	BX387097	BX387097
C 43	39.4	1.7	1055	13	BX380488	BX380488	BX380488
C 44	39.4	1.7	1201	29	CNS016DO	AL106614	Drosophila
C 45	39.2	1.7	323	9	AV871134	AV871134	AV871134

## ALIGNMENTS

RESULT 1  
CNS005TE/c  
LOCUS  
DEFINITION  
BACRI2K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION  
AL060767  
VERSION  
AL060767.1  
KEYWORDS  
GSS.  
SOURCE  
Drosophila melanogaster (fruit fly)  
ORGANISM  
Drosophila melanogaster

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of





QY	1379	UGAACAUAUUGCAACAUGAUGAUGAUAUUGGGGUUUUACACAGAAUGACUCCACAGCA	1438
Db	776	KKKRTTWTCTAAARRRRRAAAAKGTTTKTGGRRARAAAMDMWTTTTCGATTRGRGAA	717
QY	1439	CAGACAUUGCAUAUGAAGGGGUAAGUCUACGCAAAAUGGCGGUAUGAUAUA	1490
Db	716	AAATTRGCAAAAATGAGKTTDAGAAAATAAMWRRFTTMDWMAAADAAGAAW	665
RESULT 5	EX351150/c		
LOCUS	EX351150	1089 bp	mRNA
DEFINITION	EX351150 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens		
ACCESSION	EX351150		
VERSION	EX351150.1	GI:30377590	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
TAXISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1089)		
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to technology cluster 8953.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSDBAK019AB05NM1&cluster=8953.f. Contact : Peng liang Email : fliang@life.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSDBAK019AB05NM1.		
FEATURES	source		
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	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DC025YH02"		
	/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"		
	/clone_idb="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"		
	/note="First strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
	BASE COUNT	219 a 375 c 47 g 446 t	2 others
ORIGIN			
	Query Match	2.0%; Score 46; DB 13; Length 1089;	
	Best Local Similarity	36.2%; Pred. No. 11;	
	Matches	153; Conservative 41; Mismatches 226; Indels 3; Gaps 1;	
QY	1213	GAAGCAUAUUGUGCGCAUGUGUAUUUUCACAAGAAUGUGAUAUAAAGCAGUAGA	1272
Db	1009	GCATTAAGAGAAAGAAAGAGAGATGATGAGAAAGAAAGATTAAGAAATAAANGTGA	950
QY	1273	GGUGAUCUGAUAUUGGUUAUAUGGCAAAUACGCGCAUUGAACCAUACCAACUUA	1332
Db	949	GGAAGCAGATTGTGAGGACTTGATTTGATGATGGGTTTAATATTTATGTGTGTAATTA	890
QY	1333	AGACAUAUUCAGAAAGAUUGCAAAAGUCUUUUUCAAUUUGGGCAUAUUGAACAUUCAC	1392
Db	889	TAAATTTGTAGGTACGAAGTCAGAAAGGAGCAAAAAGAGAAATGAGAAATAGGAAG	830
QY	1393	AUUGUAGAGGAU---GAUUGGGUUAUACCAAGCAUAGCUCCAAAGACAGAGAUUGCA	1449
Db	829	GGGGTGTGAAATGACATGAGCGATTTATTTGAATATAGTATAGGAGAGAAAGAGAGAGC	770

Oy		1450	AUGAGAGGGGAAAGAATGCACGAATAAUAUCCGACGCCGAGAGUA	1509
Dd		769	AAAAGAGAGAAAAAGTAGAGGGGGAGAGATGAGTGTAGTGATTGGATG	710
Oy		1510	GUGUGAGCAUUAGCCGCUUUUUUUGAGGUUCGACCACAAGGAAAUUGACUA	1568
Dd		709	GTGTGAGAGTTGTTATGATTAATGAGTATGGAGAGAAAGGAGAGTGGAAAGATAT	650
Oy		1570	CTUGAGAGGTCACUAGAAACACAGGAAACAGAAACUACAAUACUACUACGCA	1629
Dd		649	GAAAGAGAGGAATGGCGTGAAGAAAGAAAGAAAGAAAGATTAAATAATATATGATTAA	590
Oy		1630 AUG 1632		
Dd		589 ATG 587		
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RESULT 6	CNS0182P		1101 bp DNA linear GSS 26-JUL-1999	
LOCUS	CNS0182P			
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37D10 of DrosBAC library, from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL108811			
VERSION	ALI08811.1 GI:5629115			
KEYWORDS	GSS.			
SOURCE ORGANISM	Drosophila melanogaster (fruit fly)			
REFERENCE	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
TITLE	Genoscope.			
JOURNAL	Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)			
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbeloBACL1.			
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FEATURES SOURCE	Location/Qualifiers			
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	/mol_type="genomic DNA"			
	/db_xref="taxon:7227"			
	/clone="BACN37D10"			
	/clone_1ib="DrosBAC"			
	/plasmid="pbeloBACL1"			
	/note="end : SP6"			
BASE COUNT	274 a 268 c 128 g 73 t 358 others			
ORIGIN				
	Query Match 2.0%; Score 45.8; DB 29; Length 1101;			
	Best Local Similarity 12.5%; Pred. No. 12;			
	Matches 38; Conservative 149; Mismatches 116; Indels 0; Gaps 0;			
Oy	1043 AGAGAGGGAAGAAAGUCUACGGCGCAUUCUCAAACAUUGAAAUUAAAGGUGCAGUACG	1102		
Dd	720 RKKKKGCGCKGAKTKTAAWAKGRKMGTATAMTWTAADVTYKAATTDPAKAAACRR	779		
Oy	1103 GAUAGCAGAGUUCACAUGGUTUGGAAAGGCAACAGCUGAUUACUGAACCAACA	1162		
Dd	780 KRDARKARBOCGRRARRRBAWMAAGCRABAPGARBARRAARDROWDMAAAAAAAAA	839		
Oy	1163 GGAGAUUGAUUCAGCUGAUUUGUGAGUGAAGACAGCAACGUGCUGAAGCAAUAA	1222		
Dd	840 AAAAWMTTRRWMDWDMDTRWDDDTTAAWWDAARAARRRRRRRRARARAAAD	899		

QY 1223 UUGUGCCAGUAGUUAUUGUAGUUAUAGAGUUAAGAGUAGUAGUAGU 1282  
 Db 900 DTTDRBADAATTTTCTTTTDDDDDDKAKRBMWAAKADGAKRRDARDMAATK 959  
 QY 1283 AUTUUGUUAUAGGCGAUAUAGCGAUUAGUUAUAGCGAUUAGUUAUAG 1342  
 Db 960 DDDGKDKMGGRGKRGKGGKRRMDGKTGKKDDDDMDKTWRDMMWTRTKMDMMDDG 1019  
 QY 1343 AGA 1345  
 Db 1020 RGR 1022

RESULT 7  
 CNS00396/c  
 LOCUS  
 DEFINITION  
 BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL063921  
 AL063921.1 GI:4941778  
 GSS.  
 Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1101)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)  
 Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see [http://www.fruitfly.org/TheBDGP/Drosophila\\_melanogaster\\_BAC\\_library](http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library) was prepared by Kazuhiro Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="BACR08K10"  
 /clone\_1lb="RPCI-98"  
 /note="Tend : TET3"  
 /note="Tend : TET3"  
 201 a 64 c 131 g 202 t 503 others

BASE COUNT  
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 Best Local Similarity 11.6%; Pred. No. 15;  
 Matches 74; Conservative 302; Mismatches 256; Indels 7; Gaps 2;

QY 998 GUTUUGCGGUGUACAUUUAAGAAAGCGAGUACUAGAGAGAGAGAGAG 1057  
 Db 1094 DDTWDDTRDDMDWTMTWTKDRADRDRAWDGAGTWTATATMTWMMWMA 1035  
 QY 1058 UGUTUACCGGCAUUCUUAACAUAUAGGUGUAGUGGGA--UACAGAGAU 1115  
 Db 1034 TWTWMDKMMWMTAAATTTATMTWTRAWADWAGDRGKRRDRAATDADGARRDG 975  
 QY 1116 CACAUGUGUGAGAAAGCGCAACGUUACUAGAAAGAGAGAGAGAGAUUUA 1175

Db 974 RKRKDKKRDGDGDDKKGKKKAATKMTWMDMDMDKMDGAKDRKADDDCA 915  
 QY 1176 GCGAUUGUAGUGGAGAGAGAGAGAGAGUAGUGUAGUUAUUGUGCCAGUGU 1235  
 Db 914 GDXDDGKGDADDDTDTGDDDDKDDMDKAKGTWGDATWMAATMDMMWADADW 855  
 QY 1236 AUUUAACAAGAGAUUGUUAUAGAGAGUUAAGUGUAGUUAUUGUUAUUG 1295  
 Db 854 WTDAAADWMAADRDWAMWMDWAMGARTDRDWDGDRGKRGARRRDRRAD 795  
 QY 1296 GCGAAUUGAGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 1355  
 Db 794 KRDAADRDADAATTTTTRDTRDTRDTRDTRDTRDTRDTRDTRDTRDTRD 740  
 QY 1356 AGUGCUUUAUUAUUGGAGUUAUUGAGUUAUUGAGUUAUUGAGUUAUUG 1415  
 Db 739 GTGGRKRRRTWKRWRKRRDTRMDADADTDADDRRRRRDGDAGKGTGKR 680  
 QY 1416 AUUACAGAGUAGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 1475  
 Db 679 ATWDRDAMWADAMWTTTDTDTDTDMDKRRRRKARRRRTTARAAWMTWKADW 620  
 QY 1476 GGGCGUAGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 1535  
 Db 619 WDKTRADRDMDADTWTDAKADBDWAKARARRRRAARADRRMTTKGTTAT 560  
 QY 1536 AGUUGAGAGCAAGAGAGAGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 1595  
 Db 559 WTWARAAWMAWMAWTTTATTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTT 500  
 QY 1596 AACAGAGAAACGAGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUGUUAUUG 1634  
 Db 499 AWTAAWMAAAWMAWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTW 461

RESULT 8  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email : seque@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by life technologies, a division of Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
 Faraday Avenue Genoscope sequence ID : CS0D1079DGO8NPL.  
 Location/Qualifiers  
 1. 1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /cissue\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  
 155 a 152 c 130 g 182 t 582 others

BASE COUNT  
 ORIGIN



	Query Match	1.9%	Score 45:	DB 13;	Length 1201;	
	Best Local Similarity	6.2%	Pred. No. 19;	Mismatches 135;	Indels 0;	Gaps 0;
	Matches 20;	Conservative 166;				
Qy	212	GAUUAACGAAAUUAUUCUGAGAAUAUGCAAGGGCAAACUCUAUGAGUAAAAUGA	271			
Db	1110	GGRRWNNMNMNMGRRGRMMVYMGGRNGGGSVVYGGGAMNNNNNNKKKNNNNKN	1051			
Qy	272	UGUAVGCCCGAUGCAGUCUGUGAUGUAUCUCUGCCUGCUGACAUGUGUGAUAUGAA	331			
Db	1050	KNNMKXDMNNMKKNMNNMKKNMNNNNMKKKMDKNNMKKKKKKKNNNNNNNNNDAA	991			
Qy	332	AUGAACCAUGACAAGUACGUGUCAUUUUCCAAUAUUCAAAACUUUAUUUGAGAAG	391			
Db	990	AAAAAKAAAAAARKKKAADAAAAAANAANNAANNNNNNNNNNNNNNNNNNNNNNN	931			
Qy	392	UCGAAAGUUAAAACUAGAACCUUUGCCGUCGUUUUUGAAGAACAAGUCAAUAC	451			
F	930	MMKMAMDKKKKMMMMMMMMTTTTTMMNNMTTMMNNMTTMMNNMTTKTTKTMM	871			
Qy	452	GCCGAGAGUUGACUAUAUUCUGUCACAGACCUCUAGCCAAAGAGCAGAGU	511			
Db	870	KNNNNHNN	811			
Qy	512	UAUUCAGGAAGUGUUTUCC	532			
Db	810	MMNTMMNKMTTMMKKBTXYM	790			
RESULT 9	CNS0006J	1101 bp	DNA	linear	GSS 03-JUN-1999	
LOCUS	Drosophila melanogaster genome survey sequence TEI3 end of BAC #					
DEFINITION	BACR01M22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.					
ACCESSION	AL062049					
VERSION	ALI062049.1					
KEYWORDS	GSS.					
SOURCE	Drosophila melanogaster (fruit fly)					
ORGANISM	Drosophila melanogaster					
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygotia; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
AUTHORS	1 (bases 1 to 1101)					
TITLE	Genoscope.					
JURNAL	Direct Submission					
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Oosagawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPac Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.					

FEATURES

SOURCE

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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR01M22"
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ORIGIN					

Query Match	1.9%	Score 44.6;	DB 29;	Length 1101;
Best Local Similarity	21.1%	Pred. No. 23;		
Matches 82;	Conservative 138;	Mismatches 164;	Indels 5;	Gaps 1;

15 AAUUAUUTCAUAUGGAAAGAUAAAAGACUACGAUUCUAUGUCGACUCCGAC 74

Db 691 AAAAAAAAAAAGGAGGAGGGRAGARARGRGGRRAAAAKTGGKKKTKTKRKA 750

75 UCGCGAUAUACUACCAAAAAACCAAGUG-----ACCAUUGGCGCAUAUAUAAGAAGUAC 129

Db 751 AGRARRRWAGAAAAAAAAAALADATKTGCTMAKAAERTAAWKCDWKADAAAAKAAART 810

[illegible]

180	TAATCCGCTTTCACCCCGCATGAGAGATTACGAAATATGCAAGGCG	249	
DB	811	KDWITAKAKDKIKWGGAAATGAGGAGAAAGKRWGRKGNLGGTAKKAKGAGGGG	870

Dbb 871 WAAWAAATTAARWDATAADDBRKKAMDRAAAAADDQDKGRRGWGTCGRRRRRARTRK 930

250 CAAACUCUAGGAGUAAAUAGAGUAGUCGCGGATCGGATCGUGUGAGUGGUATCACCTCTCG 309

Db 931 AKAKRGAGACAKAKRAKGDAMDGMKKKKWDADAAAKAKGTGDMKTPAKATGWA 990

310 GCTUGACATGCTGGAAUAGAAUAGACCAUGACCAAGUACGGTTCATUUAUCCAAAUAUC 369

```

Db      991  RADKGRRAADDTRRRTKAMWTTDWRAVATATKDKTKDKAKKGAWKTTTRIDRAAKK 105
          : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

```

QY 370 UACAAACTUATUUUGAGAAAGUCGAAAG 398  
· || ······ · · |

Db 1051 AKDDTAATRTATWKCADDKAKARDAKAK 1079

## RESULT 10

BU771589				
LOCUS	BU771589	833 bp	mRNA	linear
				EST 12-FEB-2001

DEFINITION	SJEDYG01 SJF Schistosoma japonicum cDNA, mRNA sequence.
ACCESSION	BU771589

KEYWORDS EST. BU7771589.1 GI:28338905  
VERSION  
SOURCE cshic:ccomc japonicum

ORGANISM  
SOURCE  
Schistosoma japonicum  
Schistosoma japonicum  
Ruharova: Metazoa: Platyhelminthes: Trematoda: Digenea:

REFERENCE  
1 (bases 1 to 833)

**AUTHORS**  
Hu, W., Yan, Q., Shen, D., Liu, F., Xu, X., Zhu, Z., Zhang, X., Wang, J.,  
Sun, J., Xu, X., Wang, Z., Zeng, L., Rong, Y., Wu, X., Qu, J., Xu, Z.,

Huang, J., Ma, Y., Wang, S., Wang, Z., Xue, C., Feng, Z., Chen, Z. and Han, Z.

Expressed sequence tags from eggs of *Schistosoma japonicum*  
Unpublished

COMMENT  
Contact: zeguang Han  
Chinese National Human Genome Center at Shanghai  
361 Guo Chouling Road Zhongnang Hi Tech Park Pudong Shanghai

351 GUO SHUJING ROAD, ZHANGJIANG HI TECH PARK, TAOQING, CHANGCHUN  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922  
Email: hanzg@chqc.sh.cn.

FEATURES	Location/Qualifiers
source	1. .833

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/organism="Schistosoma japonicum"
/mol_type="mRNA"

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/dd xrel="taxon:6182"  
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BASE COUNT	334 a	126 c	122 g	251 c
ORIGIN				

[illegible][illegible]

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QY	1354	AAAAGGCGUUUUUCCAAUAUUUGGGGAUUGAACUUAUCAGUAUUGUAUUGGGAUUGG	1413	1413						
Db	647	AAAAGGCGUWTTTAAAAAAYTTTTTTTGAACCGTAYTGMTATATTTCCRMAAGAMGAA	588							
QY	1414	GUUUAUCCAGACUAGCUCUCCAGACAAGAGAUUGUACUAGAGGGGUAAAGUCAGCAA	1473							
Db	587	TGGCGMAHAGRASCCAGKAMATAGMAAAAAAGACGSCACWTCGGSMTGACASAAAAC	528							
QY	1474	AUUGGCGGAGUAGUAVUACUUCUCCAGCGCGAGAGAGUAGUGUGAGAUUGAACCGUGUUUG	1533							
Db	527	GAGAMWTTTMMTTTAAACCTTTTCMTSCKATPAGGAAGGTGKMASSGTTTAAASWCAITTA	468							
QY	1534	AGAGUUCGAGACCAACGAGGAAAUAGUACUACUUCUCCUGAGAGAGUACUGUAAAACACAG	1593							
Db	467	YTTGCGCYMCRITGGTGYTRAGYRMDTGYACAAACATTTTSCBASATGCTCSMAACAGACAS	408							
QY	1594	GGAAACAGGAAACUGAGCAAUAA	1615							
Db	407	AAATTTAAACATACAAAABAAAAA	386							

RESULT 13	
AZ045148/c	
LOCUS	AZ045148
DEFINITION	Gm UMB001_133 G05R UMN Soybean BAC Library (PECSBAC4 EcoRI) Glycine max genomic clone Glycine max genomic survey sequence.
	204 bp DNA linear GSS 31-JAN-2003
	Gm_UMB001_133_G05,

ACCESSION	AZ045148	GI:791314
VERSION	AZ045148.1	
KEYWORDS	GSS.	
SOURCE	Glycine max (soybean)	
ORGANISM	Glycine max	

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaeae; Glycine.

REFERENCE	1 (bases 1 to 204)
AUTHORS	Latson, K., Mudge, J., Cooper, A., Griiva, S., Denny, R., Pennula, S., Danesn, D. and Young, N.D.
TITLE	BAC End sequences from a soybean genomic library (UMN)
JOURNAL	Unpublished
COMMENT	Contact: Young Nevin D

Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA  
Tel: 612 625 2225  
Fax: 612 625 9728  
Email: nevin@tc.umn.edu  
Sequence on contig Gm B030.ctg a near unmapped duplicate of RFP  
probe PB030. For more information, see Soybase at:  
<http://soybase.agron.iastate.edu>, please see as an authority for  
the mapping/naming: Cregan P.B., T. Jarvik, A.L. Bush, R.C.  
Sheneker, K.G. Laik, A.L. Kallier, N. Kaya, T.T. Vantolai, D.G.  
Lohmeijer, T. Chung, and J.E. Specht. 1999a. An integrated genetic  
linkage map of the soybean genome. *Crop Sci.* 39:1464-1490  
Seq primer: M13R  
Class: BAC ends.

FEATURES	Location/Qualifiers
SOURCE	1. .204

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/mol_type="genomic DNA"
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/clone_lib="UNN Soybean BAC Library (pECSBAC4 EcORI)
Glycine max genomic clone"
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Theor. Appl. Genet. 96:196, 1998) was constructed using
the Eco RI site of pECSBAC4. The library consists of 72

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BASE COUNT  
ORIGIN

71 a 21 c 20 g 85 t 7 others

Query Match	1.9%	Score 43.4	DB 28	length 204
Best Local Similarity	38.3%	Pred. 0.29		
Matches 49, Conservative	25	Mismatches	54	Indels 0
				Gaps 0

1657 UCAGUGUGGUCUACUACCUUACAGUGAUCACAGAAACUGGAAACUGUUAAAUUCAG 1716

1717 TGGUCUCAGAAUCCUACAUGCUAAUACAUAAGAUAUUGAGCCAUUUCAGUCUUA 1776

Db 123 TGATTTAAAAACCAAAATGAAATACAGTTAACTTAATTTGAGGATTTNNATGATTTT 64

Db 63 TTTCAAA 56

RESULT 14	LOCUS	DEFINITION
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BX376097		RNA
BX376097		Homo sapiens NEUROBLASTOMA COT 25 NORMALIZED Homo sapiens
CNA clone CS0DC022YM12		5-PRIME, mRNA sequence.

ACCESSION	BX376097	GI:30434756
VERSION	BX376097.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE  
1 (bases 1 to 1201)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**AUTHORS** Li, W. B., Gruber, C., Jasssee, J. and Polayres, D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished  
**COMMENT** Contact: Genoscope

Genoscope - Centre National de Séquençage  
BP 191 91006 EVRY cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by life technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 2866.f  
Contact : Feng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL :  
<http://fulllength.invitrogen.com/invitrogen/Corporation> 1600  
Faraday Avenue Genoscope sequence ID : CS00C02BBG66Q01.

FEATURES	Location/Qualifiers
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
ORIGIN
79 a      152 c      66 g      270 t      634 others

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				1;	Gaps 1;
Oy	312 UGUCAGUGGUGGAUUGAUAUGACCAACAUAUGCAGTUTAUUUCCAAAAATUCA	371			
D6	1074 KRKDAADGGKAAKAWAGAACAGAAGAGAGGCKGGKAALKRTTTTKTRNNNNNNNNNNN	1015			

